OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: October 12, 2004, 09:34:09

Title: US-10-619-910-11
Perfect score: 111
Sequence: 1 INPETVPKPCCAPTQLNAIS 20

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents AA:*
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               2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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               6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

; Search time 23 Seconds
; (without alignments)
; 44.892 Million cell updates/sec

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	111	100.0	20	4	US-09-439-779B-11	Sequence 11, Appl
2	111	100.0	102	4	US-08-335-583C-47	Sequence 47, Appl
3	111	100.0	102	2	US-08-288-508C-18	Sequence 18, Appl
4	111	100.0	102	3	US-08-478-097A-16	Sequence 16, Appl
5	111	100.0	102	3	US-08-289-222B-27	Sequence 27, Appl
6	111	100.0	102	3	US-08-054-526B-27	Sequence 27, Appl
7	111	100.0	102	3	US-08-931-858B-161	Sequence 161, App
8	111	100.0	102	3	US-08-981-739-161	Sequence 161, Appl
9	111	100.0	102	3	US-08-786-284A-1	Sequence 1, Appl
10	111	100.0	102	3	US-09-128-026-161	Sequence 161, App
11	111	100.0	102	4	US-09-496-398-16	Sequence 16, App
12	111	100.0	102	4	US-09-220-616-161	Sequence 161, App
13	111	100.0	104	4	US-09-374-956C-55	Sequence 55, Appl
14	111	100.0	104	4	US-07-764-731B-8	Sequence 8, Appl
15	111	100.0	117	4	US-09-374-956C-69	Sequence 69, Appl
16	111	100.0	118	2	US-08-481-377-12	Sequence 12, Appl
17	111	100.0	118	2	US-08-491-835-10	Sequence 10, Appl
18	111	100.0	118	3	US-09-153-573A-12	Sequence 12, Appl
19	111	100.0	118	3	US-08-946-092A-10	Sequence 10, Appl
20	111	100.0	118	3	US-09-172-062-10	Sequence 10, Appl
21	111	100.0	118	3	US-09-301-520D-10	Sequence 10, Appl
22	111	100.0	118	4	US-09-389-705-12	Sequence 12, Appl
23	111	100.0	118	5	PCT-US94-00666-12	Sequence 12, Appl
24	111	100.0	118	5	PCT-US94-00685-10	Sequence 10, Appl
25	111	100.0	118	5	PCT-US-581-529B-12	Sequence 12, Appl
26	111	100.0	119	1	US-08-455-559-18	Sequence 18, Appl
27	111	100.0	119	2	US-08-525-596B-22	Sequence 22, Appl
28	111	100.0	119	2	US-08-581-528A-12	Sequence 12, Appl
29	111	100.0	119	3	US-09-097-616-12	Sequence 12, Appl
30	111	100.0	119	3	US-09-177-860A-22	Sequence 22, Appl
31	111	100.0	119	3	US-08-624-635-13	Sequence 13, Appl
32	111	100.0	119	3	US-08-289-222B-27	Sequence 27, Appl
33	111	100.0	119	4	US-09-145-060-18	Sequence 18, Appl
34	111	100.0	119	4	US-09-378-238-26	Sequence 26, Appl
35	111	100.0	119	4	US-09-629-938-22	Sequence 22, Appl
36	111	100.0	119	4	US-09-686-344-40	Sequence 40, Appl
37	111	100.0	119	5	PCT-US94-07762-12	Sequence 12, Appl
38	111	100.0	119	5	PCT-US94-07799-12	Sequence 12, Appl
39	111	100.0	119	5	US-07-718-274A-2	Sequence 2, Appl
40	111	100.0	119	5	US-08-163-877-10	Sequence 10, Appl
41	111	100.0	139	1	US-08-149-106-2	Sequence 2, Appl
>42	111	100.0	139	1	US-08-298-021-2	Sequence 2, Appl
>43	111	100.0	139	1	US-09-412-791D-12	Sequence 12, Appl
44	111	100.0	139	1	US-08-278-729A-5	Sequence 5, Appli
45	111	100.0	139	1	US-08-155-343A-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-439-779B-11
; Sequence 11, Application US/09439779B
; Patent No. 6617307
; GENERAL INFORMATION:
; APPLICANT: Kyocera Corporation
; APPLICANT: Nishimura, Yoshihiko
; APPLICANT: Suzuki, Yoshihisa
; APPLICANT: Tanihara, Masao
; TITLE OF INVENTION: A Peptide and Osteogenetic Accelerator
; FILE REFERENCE: 81918-0001
; CURRENT APPLICATION NUMBER: US/09/439,779B
; CURRENT FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.1
;
; SEQ ID NO 11
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-439-779B-11

Query Match   100.0%; Score 111; DB 4; Length 20;
Best Local Similarity 100.0%;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 INPETVPKPCCAPTQLNAIS 20
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Db   1 INPETVPKPCCAPTQLNAIS 20

RESULT 2
US-08-335-583C-47
; Sequence 47, Application US/08335583C
; Patent No. 5693779
; GENERAL INFORMATION:
; APPLICANT: Moos Jr., Malcolm
; APPLICANT: Wang, Shouwan
; APPLICANT: Krinks, Marie
; TITLE OF INVENTION: PRODUCTION AND USE OF
; TITLE OF INVENTION: ANTI-DORSALIZING MORPHOGENETIC PROTEIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,583C
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: NIH104.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
TELEX:
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ANTI-SENSE: NO
HYPOTHETICAL: NO
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
US-08-335-583C-47

Query Match   100.0%;   Score 111;   DB 1;   Length 102;
Best Local Similarity   100.0%;   Pred. No. 4.3e-08;
Matches 20;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy   1  INPETVPKPCCAPTQLNAIS  20
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Db  57  INPETVPKPCCAPTQLNAIS  76
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RESULT 3
US-08-288-508C-18
Sequence 18, Application US/08288508C
Patent No. 5994094
GENERAL INFORMATION:
APPLICANT: H tten, Gertrud
APPLICANT: Neidhardt, Helge
APPLICANT: Paulista, Michael
TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATING FACTOR OF
TITLE OF INVENTION: THE TGF- FAMILY
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
STREET: 655 Fifteenth Street N.W. Suite 330
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/288,508C
FILING DATE: 10-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 435
FILING DATE: 10-AUG-1994
CLASSIFICATION:
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 44 18 222.8
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 20 157.5
FILING DATE: 09-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jahns, Kristina M.
REGISTRATION NUMBER: P-41,092
REFERENCE/DOCKET NUMBER: P564-4019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
TELEFAX: (202)638-4810
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-288-508C-18

Query Match   100.0%;   Score 111;   DB 2;   Length 102;
Best Local Similarity   100.0%;   Pred. No. 4.3e-08;
Matches 20;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy   1  INPETVPKPCCAPTQLNAIS  20
        |||||||||||||||||||||
Db  57  INPETVPKPCCAPTQLNAIS  76
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RESULT 4
US-08-478-097A-16
Sequence 16, Application US/08478097A
Patent No. 6040431
GENERAL INFORMATION:
APPLICANT: KECK, PETER
APPLICANT: SMART, JOHN
TITLE OF INVENTION: SINGLE-CHAIN ANALOGS OF TGF-B
TITLE OF INVENTION: SUPERFAMILY (MORPHONS)
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR; TESTA, HURWITZ &
ADDRESSEE: THIBEAULT, LLP
STREET: 125 HIGH STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,097A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ., EDMND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-080
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..102

; OTHER INFORMATION: /note= "OP-1 SEQUENCE"
US-08-478-097A-16

Query Match   100.0%; Score 111; DB 3; Length 102;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 INPETVPKPCCAPTQLNAIS 20
         ||||||||||||||||||||
Db   57 INPETVPKPCCAPTQLNAIS 76

RESULT 5
US-08-289-222E-27
; Sequence 27, Application US/08289222E
; Patent No. 6120760
; GENERAL INFORMATION:
; APPLICANT: HOTTEN, GERTRUD
; APPLICANT: NEIDHARDT, HELGE
; APPLICANT: BECHTOLD, ROLF
; APPLICANT: POHL, JENS
; TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B
; TITLE OF INVENTION: FAMILY
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM
; STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
; STREET: SUITE 330
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/289,222E
; FILING DATE: 25-AUG-1999
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,222
; FILING DATE: 12-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 23 190.3
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EPO 92102324.8
; FILING DATE: 12-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00350
; FILING DATE: 12-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KITTS, MONICA CHIN
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P564-9021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-289-222B-27

Query Match   100.0%; Score 111; DB 3; Length 102;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 INPETVPKPCCAPTQLNAIS 20
         ||||||||||||||||||||
Db   57 INPETVPKPCCAPTQLNAIS 76

RESULT 6
US-09-054-526B-27
; Sequence 27, Application US/09054526B
; Patent No. 6197550
; GENERAL INFORMATION:
; APPLICANT: H TTEN, GERTRUD
; APPLICANT: NEIDHARDT, HELGE
; APPLICANT: BECHTOLD, ROLF
; APPLICANT: POHL, JENS
; TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
; TITLE OF INVENTION: GROWTH/DIFFERENTATION FACTORS
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
; STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
; STREET: SUITE 330
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,526B
; FILING DATE: 03-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,222
; FILING DATE: 12-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 23 190.3
; FILING DATE: 01-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EPO 92102324.8
; FILING DATE: 12-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00350
; FILING DATE: 12-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KITTS, MONICA CHIN
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P564-8005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-054-526B-27

Query Match   100.0%; Score 111; DB 3; Length 102;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 INPETVPKPCCAPTQLNAIS 20
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Db   57 INPETVPKPCCAPTQLNAIS 76

RESULT 7
US-08-931-858E-161
; Sequence 161, Application US/08931858E

; Patent No. 6222022
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, EUGENE M
; APPLICANT: MILBRANDT, JEFFREY D
; APPLICANT: KOTZBAUER, PAUL T
; APPLICANT: LAMPE, PATRICIA A
; APPLICANT: KLEIN, ROBERT
; APPLICANT: DESAUVAGE, FRED
; TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MO
; ZIP: 63105
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/931,858E
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 971486
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 161:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-931-858E-161

Query Match   100.0%;   Score 111;   DB 3;   Length 102;
Best Local Similarity   100.0%;   Pred. No. 4.3e-08;
Matches 20;   Conservative 0; Mismatches 0;   Indels 0;   Gaps 0;

Qy   1 INPETVPKPCCAPTQLNAIS 20
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Db   57 INPETVPKPCCAPTQLNAIS 76

RESULT 8
US-08-981-739-161
; Sequence 161, Application US/0898l739
; Patent No. 6232449
; GENERAL INFORMATION:
; APPLICANT: JOHNSON JR., EUGENE M.
; MILBRANDT, JEFFREY D.
; KOTZBAUER, PAUL T.
; LAMPE, PATRICIA A.
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: US
; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
; NUMBER OF SEQUENCES: 176

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,739
; FILING DATE: 31-Aug-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/03461
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 976163
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 161:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 161:
US-08-981-739-161

Query Match   100.0%;   Score 111;   DB 3;   Length 102;
Best Local Similarity   100.0%;   Pred. No. 4.3e-08;
Matches 20;   Conservative 0; Mismatches 0;   Indels 0;   Gaps 0;

Qy   1 INPETVPKPCCAPTQLNAIS 20
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Db   57 INPETVPKPCCAPTQLNAIS 76

RESULT 9
US-08-786-284A-1
; Sequence 1, Application US/0878628 4A
; Patent No. 6273598
; GENERAL INFORMATION:
; APPLICANT: KECK, PETER
; APPLICANT: GRIFFITH, DIANA L
; APPLICANT: CARLSON, WILLIAM L
; APPLICANT: RUEGER, DAVID C
; APPLICANT: SAMPATH, KUBER T
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PRODUCING
; TITLE OF INVENTION: MORPHOGEN ANALOGS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,
; ADDRESSEE: INC
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/786,284A
; FILING DATE:
; CLASSIFICATION: 364
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 435-9001
; TELEFAX: (508) 435-0992
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

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;   LENGTH: 102 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   FEATURE:
;     NAME/KEY: Protein
;     LOCATION: 1..102
;     OTHER INFORMATION: /product= "hOP-1"
US-08-786-284A-1

Qy   1 INPETVPKPCCAPTQLNAIS 20
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Db  57 INPETVPRCCAPTQLNAIS 76

Query Match             100.0%;  Score 111;  DB 3;  Length 102;
Best Local Similarity   100.0%;  Pred. No. 4.3e-08;
Matches  20;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

US-09-128-026-161
RESULT 10
US-09-128-026-161
Sequence 161, Application US/09128026
Patent No. 6403335
GENERAL INFORMATION:
  APPLICANT: JOHNSON JR., EUGENE M.
  APPLICANT: MILBRANDT, JEFFREY D.
  APPLICANT: KOTZBAUER, PAUL T.
  APPLICANT: LAMPE, PATRICIA A.
  TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
  NUMBER OF SEQUENCES: 176
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: HOWELL & HAFERKAMP, L.C.
    STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
    CITY: ST. LOUIS
    STATE: MISSOURI
    COUNTRY: US
    ZIP: 63105-1817
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/128,026
    FILING DATE:
    CLASSIFICATION:
  ATTORNEY/AGENT INFORMATION:
    NAME: HOLLAND, DONALD R.
    REGISTRATION NUMBER: 35,197
    REFERENCE/DOCKET NUMBER: 976163
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (314) 727-5188
    TELEFAX: (314) 727-6092
  INFORMATION FOR SEQ ID NO: 161:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 102 amino acids
    TYPE: amino acid
    STRANDEDNESS: single
    TOPOLOGY: linear
    MOLECULE TYPE: peptide
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Qy   1 INPETVPKPCCAPTQLNAIS 20
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Db  57 INPETVPRCCAPTQLNAIS 76

Query Match             100.0%;  Score 111;  DB 4;  Length 102;
Best Local Similarity   100.0%;  Pred. No. 4.3e-08;
Matches  20;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

US-09-128-026-161
RESULT 11
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US-09-496-398-16
Sequence 16, Application US/09496398
Patent No. 6479643
GENERAL INFORMATION:
  APPLICANT: KECK, PETER
  APPLICANT: SMART, JOHN
  TITLE OF INVENTION: SINGLE CHAIN ANALOGS OF TGF-B
  TITLE OF INVENTION: SUPERFAMILY (MORPHONS)
  NUMBER OF SEQUENCES: 45
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: PATENT ADMINISTRATOR; TESTA, HURWITZ &
    ADDRESSEE: THIBEAULT, LLP
    STREET: 125 HIGH STREET
    CITY: BOSTON
    STATE: MA
    COUNTRY: USA
    ZIP: 02110
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.25
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/478,097
    FILING DATE: 07-JUN-1995
    CLASSIFICATION:
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/496,398
    FILING DATE:
    CLASSIFICATION:
  ATTORNEY/AGENT INFORMATION:
    NAME: PITCHER ESQ, EDMUND R
    REGISTRATION NUMBER: 27,829
    REFERENCE/DOCKET NUMBER: STK-059CN
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 617-248-7000
    TELEFAX: 617-248-7100
  INFORMATION FOR SEQ ID NO: 16:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 102 amino acids
    TYPE: amino acid
    STRANDEDNESS: single
    TOPOLOGY: linear
    MOLECULE TYPE: protein
  FEATURE:
    NAME/KEY: Protein
    LOCATION: 1..102
    OTHER INFORMATION: /note= "OP-1 SEQUENCE"
US-09-496-398-16

Qy   1 INPETVPKPCCAPTQLNAIS 20
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Db  57 INPETVPRCCAPTQLNAIS 76

Query Match             100.0%;  Score 111;  DB 4;  Length 102;
Best Local Similarity   100.0%;  Pred. No. 4.3e-08;
Matches  20;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

US-09-220-616-161
RESULT 12
US-09-220-616-161
Sequence 161, Application US/09220616
Patent No. 6645937
GENERAL INFORMATION:
  APPLICANT: JOHNSON JR., EUGENE M.
  APPLICANT: MILBRANDT, JEFFREY D.
  APPLICANT: KOTZBAUER, PAUL T.
  APPLICANT: LAMPE, PATRICIA A.
  TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
  NUMBER OF SEQUENCES: 176
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: HOWELL & HAFERKAMP, L.C.
    STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
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;   CITY: ST. LOUIS
;   STATE: MISSOURI
;   COUNTRY: US
;   ZIP: 63105-1817
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/220,616
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/981,739
;   FILING DATE: 31-Aug-1998
;   APPLICATION NUMBER: PCT/US97/03461
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: HOLLAND, DONALD R.
;   REGISTRATION NUMBER: 35,197
;   REFERENCE/DOCKET NUMBER: 976163
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (314) 727-6092
;   TELEFAX: (314) 727-5188
;   INFORMATION FOR SEQ ID NO: 161:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 102 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-09-220-616-161

Qy    1 INPETVPKPCCAPTQLNAIS 20
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Db   57 INPETVPKPCCAPTQLNAIS 76

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Best Local Similarity   100.0%;   Pred. No. 4.3e-08;
Matches   20;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;


RESULT 13
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;   Sequence 55, Application US/09374958C
;   Patent No. 6677432
;   GENERAL INFORMATION:
;   APPLICANT: Stryker Corporation
;   TITLE OF INVENTION: Modified Proteins and DNAs of the TGF-beta Superfamily, Including
;   TITLE OF INVENTION: Modified Morphogenic Proteins
;   FILE REFERENCE: STK-076
;   CURRENT APPLICATION NUMBER: US/09/374,958C
;   CURRENT FILING DATE: 1999-08-16
;   NUMBER OF SEQ ID NOS: 90
;   SOFTWARE: Patentin version 2.0
;   SEQ ID NO 55
;   LENGTH: 102
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: OP-1
US-09-374-958C-55

Query Match             100.0%;   Score 111;   DB 4;   Length 102;
Best Local Similarity   100.0%;   Pred. No. 4.3e-08;
Matches   20;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy    1 INPETVPKPCCAPTQLNAIS 20
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Db   57 INPETVPKPCCAPTQLNAIS 76


RESULT 14
US-07-764-731B-8
;   Sequence 8, Application US/07764731B
;   Patent No. 5366875
;   GENERAL INFORMATION:
;   APPLICANT: Rosen, Vicki A.
;   APPLICANT: Wang, Elizabeth A.
;   APPLICANT: Wozney, John M.
;   TITLE OF INVENTION: Methods for Producing BMP-7 Proteins
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
;   STREET: 87 CambridgePark Drive
;   CITY: Cambridge
;   STATE: MA
;   COUNTRY: USA
;   ZIP: 02140
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/07/764,731B
;   FILING DATE: 19910924
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Kapinos, Ellen J.
;   REGISTRATION NUMBER: 32,245
;   REFERENCE/DOCKET NUMBER: GI51159B
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617-876-1170
;   TELEFAX: 617-876-5851
;   INFORMATION FOR SEQ ID NO: 8:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 104 amino acids
;   TYPE: AMINO ACID
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-07-764-731B-8

Query Match             100.0%;   Score 111;   DB 1;   Length 104;
Best Local Similarity   100.0%;   Pred. No. 4.4e-08;
Matches   20;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy    1 INPETVPKPCCAPTQLNAIS 20
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RESULT 15
US-09-374-958C-69
;   Sequence 69, Application US/09374958C
;   Patent No. 6677432
;   GENERAL INFORMATION:
;   APPLICANT: Stryker Corporation
;   TITLE OF INVENTION: Modified Proteins and DNAs of the TGF-beta Superfamily, Including
;   TITLE OF INVENTION: Modified Morphogenic Proteins
;   FILE REFERENCE: STK-076
;   CURRENT APPLICATION NUMBER: US/09/374,958C
;   CURRENT FILING DATE: 1999-08-16
;   NUMBER OF SEQ ID NOS: 90
;   SOFTWARE: Patentin version 2.0
;   SEQ ID NO 69
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Trypsin truncated H2223 mutant
US-09-374-958C-69

Query Match             100.0%;   Score 111;   DB 4;   Length 117;
Best Local Similarity   100.0%;   Pred. No. 4.9e-08;
Matches   20;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy    1 INPETVPKPCCAPTQLNAIS 20
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Db   57 INPETVPKPCCAPTQLNAIS 76
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Matches   20;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1   INPETVPKPCCAPTQLNAIS 20
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Search completed: October 12, 2004, 09:38:46
Job time : 24 secs

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OM protein - protein search, using sw model

                              GenCore version 5.1.6
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Run on:          October 12, 2004, 09:37:49 ; Search time 96 Seconds
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Perfect score:   111
Sequence:        1 INPETVPKPCCAPTQLNAIS 20

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Searched:        1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters:    1351062

Post-processing: Minimum Match 0%
                 Maximum Match 100%
Minimum DB seq length: 0
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Database :       Published Applications AA:*
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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1	100.0	111	20	12	US-10-619-910-11	Sequence 11, Appl
2	100.0	111	97	11	US-09-754-831A-39	Sequence 39, Appl
3	100.0	111	102	9	US-09-791-946-1	Sequence 1, Appli
4	100.0	111	102	14	US-10-187-394-16	Sequence 16, Appli
5	100.0	111	102	14	US-10-164-279-4	Sequence 4, Appli
6	100.0	111	107	11	US-09-754-831A-9	Sequence 9, Appli
7	100.0	111	112	9	US-09-813-398-30	Sequence 30, Appl
8	100.0	111	118	13	US-09-813-398-10	Sequence 10, Appl
9	100.0	111	118	14	US-10-154-333-12	Sequence 12, Appl
10	100.0	111	118	16	US-10-704-223-10	Sequence 10, Appl
11	100.0	111	119	9	US-09-813-459-13	Sequence 13, Appl
12	100.0	111	119	9	US-09-859-211-40	Sequence 40, Appl
13	100.0	111	119	9	US-09-880-708-18	Sequence 18, Appl
14	100.0	111	119	10	US-09-872-856-40	Sequence 40, Appl
15	100.0	111	119	12	US-10-463-973-40	Sequence 40, Appl

ALIGNMENTS

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16 | 111 | 100.0 | 119 | 12 | US-10-693-536-12 | Sequence 12, Appl
17 | 111 | 100.0 | 119 | 14 | US-10-335-483-22 | Sequence 22, Appl
18 | 111 | 100.0 | 119 | 16 | US-10-758-210-12 | Sequence 12, Appl
19 | 111 | 100.0 | 119 | 8 | US-08-260-675-5 | Sequence 5, Appl
20 | 111 | 100.0 | 139 | 9 | US-09-882-875A-1 | Sequence 1, Appli
21 | 111 | 100.0 | 139 | 12 | US-09-952-318A-5 | Sequence 5, Appli
22 | 111 | 100.0 | 139 | 12 | US-10-366-345-63 | Sequence 63, Appli
23 | 111 | 100.0 | 139 | 14 | US-10-050-050-5 | Sequence 5, Appli
24 | 111 | 100.0 | 139 | 15 | US-1-108-260A-2783 | Sequence 2783, Ap
25 | 111 | 100.0 | 139 | 16 | US-10-385-064-5 | Sequence 5, Appli
26 | 111 | 100.0 | 161 | 9 | US-09-765-527-249 | Sequence 249, App
27 | 111 | 100.0 | 161 | 9 | US-09-760-397-2 | Sequence 2, Appli
28 | 111 | 100.0 | 169 | 14 | US-10-324-182-2 | Sequence 2, Appli
29 | 111 | 100.0 | 169 | 8 | US-08-957-425-9 | Sequence 9, Appli
30 | 111 | 100.0 | 169 | 12 | US-10-321-799-9 | Sequence 9, Appli
31 | 111 | 100.0 | 169 | 16 | US-10-428-997A-9 | Sequence 9, Appli
32 | 111 | 100.0 | 178 | 9 | US-09-760-397-8 | Sequence 8, Appli
33 | 111 | 100.0 | 178 | 14 | US-10-324-182-8 | Sequence 8, Appli
34 | 111 | 100.0 | 179 | 9 | US-09-765-527-257 | Sequence 257, App
35 | 111 | 100.0 | 179 | 9 | US-09-765-527-261 | Sequence 261, App
36 | 111 | 100.0 | 190 | 9 | US-09-765-527-255 | Sequence 255, App
37 | 111 | 100.0 | 190 | 14 | US-10-324-182-14 | Sequence 14, Appl
38 | 111 | 100.0 | 194 | 9 | US-09-765-527-263 | Sequence 263, App
39 | 111 | 100.0 | 195 | 9 | US-09-765-527-11 | Sequence 11, Appl
40 | 111 | 100.0 | 317 | 8 | US-08-957-425-11 | Sequence 11, Appl
41 | 111 | 100.0 | 317 | 12 | US-10-321-799-11 | Sequence 11, Appl
42 | 111 | 100.0 | 317 | 16 | US-10-428-997A-11 | Sequence 11, Appl
43 | 111 | 100.0 | 408 | 8 | US-08-957-425-15 | Sequence 15, Appl
44 | 111 | 100.0 | 408 | 12 | US-10-321-799-15 | Sequence 15, Appl
45 | 111 | 100.0 | 408 | 16 | US-10-428-997A-15 | Sequence 15, Appl
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RESULT 1
US-10-619-910-11

;  Sequence 11, Application US/10619910
;  Publication No. US2004005384441
;  GENERAL INFORMATION:
;  APPLICANT: Kyocera Corporation
;  APPLICANT: Nishimura, Yoshihiko
;  APPLICANT: Suzuki, Yoshihisa
;  APPLICANT: Tanihara , Masao
;  TITLE OF INVENTION: A Peptide and Osteogenetic Accelerator
;  FILE REFERENCE: 81918-0001
;  CURRENT APPLICATION NUMBER: US/10/619,910
;  CURRENT FILING DATE:  2003-07-15
;  PRIOR APPLICATION NUMBER: US/09/439,779B
;  PRIOR FILING DATE: 2001-09-10
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: Patentin version 3.1
;  SEQ ID NO 11
;  LENGTH: 20
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: :
US-10-619-910-11

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  Best Local Similarity  100.0%;  Pred. No. 7.4e-08;
  Matches 20;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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Db          1 INPETVPKPCCAPTQLNAIS 20


RESULT 2
US-09-754-831A-39

;  Sequence 39, Application US/09754831A
;  Publication No. US2003022834541
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GENERAL INFORMATION:
; APPLICANT: Oppermann, Herman
; APPLICANT: Kuberasampath, Thangavel
; APPLICANT: Rueger, David
; APPLICANT: Ozkaynak, Engin
; TITLE OF INVENTION: Osteogenic Devices
; FILE REFERENCE: STK-008CN
; CURRENT APPLICATION NUMBER: US/09/754,831A
; CURRENT FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: US 08/375,901
; PRIOR FILING DATE: 1995-01-20
; PRIOR APPLICATION NUMBER: US 08/145,812
; PRIOR FILING DATE: 1993-11-01
; PRIOR APPLICATION NUMBER: US 07/995,345
; PRIOR FILING DATE: 1992-12-22
; PRIOR APPLICATION NUMBER: US 07/315,342
; PRIOR FILING DATE: 1989-02-23
; PRIOR APPLICATION NUMBER: US 07/232,630
; PRIOR FILING DATE: 1988-08-15
; PRIOR APPLICATION NUMBER: US 07/179,406
; PRIOR FILING DATE: 1988-04-08
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin version 3.0
;
; SEQ ID NO 39
; LENGTH: 97
; TYPE: PRT
; ORGANISM: mammalian
; FEATURE:
; OTHER INFORMATION: OP1 shorter sequence capable of inducing endochondral bone format

Qy   1 INPETVPKPCCAPTQLNAIS 20
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Db   52 INPETVPKPCCAPTQLNAIS 71

Query Match   100.0%;   Score 111; DB 11; Length 97;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-754-831A-39

RESULT 3
US-09-791-946-1
Sequence 1, Application US/09791946
Patent No. US2002028453A1
GENERAL INFORMATION:
; APPLICANT: KECK, PETER
;   GRIFFITH, DIANA L
;   CARLSON, WILLIAM D
;   RUEGER, DAVID C
;   SAMPATH, KUBER T
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PRODUCING
;   MORPHOGEN ANALOGS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,
;   INC.
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/791,946
; FILING DATE: 22-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/786,284
; FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 435-9001
; TELEFAX: (508) 435-0992
INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..102
; OTHER INFORMATION: /product= "hOP-1"
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Qy   1 INPETVPKPCCAPTQLNAIS 20
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Db   57 INPETVPKPCCAPTQLNAIS 76

Query Match   100.0%;   Score 111; DB 9; Length 102;
Best Local Similarity 100.0%; Pred. No. 3.5e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
US-10-187-394-16
Sequence 16, Application US/10187394
Publication No. US20030176667A1
GENERAL INFORMATION:
; APPLICANT: KECK, PETER
; APPLICANT: SMART, JOHN
; TITLE OF INVENTION: SINGLE CHAIN ANALOGS OF TGF-B
; TITLE OF INVENTION: SUPERFAMILY (MORPHONS)
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
;   THIBEAULT, LLP
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/187,394
; FILING DATE: 28-JUNE-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/496,398
; FILING DATE: 02-FEB-2000
; CLASSIFICATION:
; APPLICATION NUMBER: US 08/478,097
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESQ, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: STK-059CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7000
; TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:

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          LENGTH: 102 amino acids
          TYPE: amino acid
          STRANDEDNESS: single
          TOPOLOGY: linear
          MOLECULE TYPE: protein
          FEATURE:
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              LOCATION: 1..102
              OTHER INFORMATION: /note= "OP-1 SEQUENCE"
US-10-187-394-16

Qy    1 INPETVPKPCCAPTQLNAIS 20
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Db   57 INPETVPKPCCAPTQLNAIS 76
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Query Match    100.0%;  Score 111; DB 14;  Length 102;
Best Local Similarity  100.0%;  Pred. No. 3.5e-07;
Matches 20;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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RESULT 5
US-10-164-279-4
Sequence 4, Application US/10164279
Publication No. US20030185792A1
GENERAL INFORMATION:
     APPLICANT: Keck, P.
     TITLE OF INVENTION: MORPHOGEN ANALOGS OF BOND MORPHOGENIC PROTEINS
     FILE REFERENCE: CIBT-PC04-566
     CURRENT APPLICATION NUMBER: US/10/164,279
     CURRENT FILING DATE: 2002-06-06
     PRIOR APPLICATION NUMBER: 09/791946
     PRIOR FILING DATE: 2001-02-22
     NUMBER OF SEQ ID NOS: 64
     SOFTWARE: Patentin version 3.1
     SEQ ID NO 4
     LENGTH: 102
     TYPE: PRT
     ORGANISM: Homo sapiens
US-10-164-279-4

Qy    1 INPETVPKPCCAPTQLNAIS 20
        ||||||||||||||||||||
Db   57 INPETVPKPCCAPTQLNAIS 76
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```
Query Match    100.0%;  Score 111; DB 14;  Length 102;
Best Local Similarity  100.0%;  Pred. No. 3.5e-07;
Matches 20;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
```

```
RESULT 6
US-09-754-831A-9
Sequence 9, Application US/09754831A
Publication No. US20030228345A1
GENERAL INFORMATION:
     APPLICANT: Oppermann, Herman
     APPLICANT: Kuberasampath, Thangavel
     APPLICANT: Rueger, David
     APPLICANT: Ozkaynak, Engin
     TITLE OF INVENTION: Osteogenic Devices
     FILE REFERENCE: STK-008CN
     CURRENT APPLICATION NUMBER: US/09/754,831A
     CURRENT FILING DATE: 2001-01-03
     PRIOR APPLICATION NUMBER: US 08/375,901
     PRIOR FILING DATE: 1995-01-20
     PRIOR APPLICATION NUMBER: US 08/145,812
     PRIOR FILING DATE: 1993-11-01
     PRIOR APPLICATION NUMBER: US 07/995,345
     PRIOR FILING DATE: 1992-12-22
     PRIOR APPLICATION NUMBER: US 07/315,342
     PRIOR FILING DATE: 1989-02-23
     PRIOR APPLICATION NUMBER: US 07/232,630
     PRIOR FILING DATE: 1988-08-15
     PRIOR APPLICATION NUMBER: US 07/179,406
     PRIOR FILING DATE: 1988-04-08
     NUMBER OF SEQ ID NOS: 72
     SOFTWARE: Patentin version 3.0
     SEQ ID NO 9
     LENGTH: 107
     TYPE: PRT
     ORGANISM: mammalian
     FEATURE:
     OTHER INFORMATION: OP1 protein sequence with osteogenic activity
US-09-754-831A-9

Qy    1 INPETVPKPCCAPTQLNAIS 20
        ||||||||||||||||||||
Db   62 INPETVPKPCCAPTQLNAIS 81
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Query Match    100.0%;  Score 111; DB 11;  Length 107;
Best Local Similarity  100.0%;  Pred. No. 3.6e-07;
Matches 20;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
```

```
RESULT 7
US-09-813-398-30
Sequence 30, Application US/09813398
Patent No. US20020169292A1
GENERAL INFORMATION:
     APPLICANT: Bruce D. Weintraub
     APPLICANT: Mariusz W. Szkudlinski
     APPLICANT: University of Maryland
     TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
     FILE REFERENCE: UOFMD.C03C1
     CURRENT APPLICATION NUMBER: US/09/813,398
     CURRENT FILING DATE: 2001-03-20
     PRIOR APPLICATION NUMBER: PCT/US99/05908
     PRIOR FILING DATE: 1999-03-19
     PRIOR APPLICATION NUMBER: PCT/US98/19772
     PRIOR FILING DATE: 1998-09-22
     NUMBER OF SEQ ID NOS: 41
     SOFTWARE: FastSEQ for Windows Version 4.0
     SEQ ID NO 30
     LENGTH: 112
     TYPE: PRT
     ORGANISM: HOMO SAPIEN
US-09-813-398-30

Qy    1 INPETVPKPCCAPTQLNAIS 20
        ||||||||||||||||||||
Db   68 INPETVPKPCCAPTQLNAIS 87
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```
Query Match    100.0%;  Score 111; DB 9;  Length 112;
Best Local Similarity  100.0%;  Pred. No. 3.8e-07;
Matches 20;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
```

```
RESULT 8
US-10-115-406-10
Sequence 10, Application US/10115406
Publication No. US20020127612A1
GENERAL INFORMATION:
     APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
     APPLICANT: LEE, Se-Jin
     TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
     FILE REFERENCE: JHU1190-3
     CURRENT APPLICATION NUMBER: US/10/115,406
     CURRENT FILING DATE: 2002-04-02
     PRIOR APPLICATION NUMBER: 09/301,520
     PRIOR FILING DATE: 1999-04-28
     PRIOR APPLICATION NUMBER: US 09/172,062
     PRIOR FILING DATE: 1998-10-13
     PRIOR APPLICATION NUMBER: US 08/491,835
     PRIOR FILING DATE: 1995-10-23
     PRIOR APPLICATION NUMBER: PCT/US94/00685
     PRIOR FILING DATE: 1994-01-12
     PRIOR APPLICATION NUMBER: US 08/003,303
```

```
PRIOR FILING DATE: 1993-01-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.0
SEQ ID NO 10
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
US-10-115-406-10
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Query Match   100.0%; Score 111; DB 13; Length 118;
Best Local Similarity   100.0%; Pred. No. 4e-07;
Matches   20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    1 INPETVPKPCCAPTQLNAIS 20
        ||||||||||||||||||||
Db   73 INPETVPKPCCAPTQLNAIS 92
```

RESULT 9
US-10-154-333-12
Sequence 12, Application US/10154333
Publication No. US20030109684A1
GENERAL INFORMATION:
APPLICANT: JOHNS HOPKINS UNIVERSITY
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: US
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/154,333
FILING DATE: 21-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/389,705
FILING DATE: 03-Sep-1999
APPLICATION NUMBER: 09/153,733
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR., Ph.D., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD2279 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: OP-1
FEATURE:
NAME/KEY: Protein
LOCATION: 1..118
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-154-333-12
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Query Match              100.0%; Score 111; DB 14; Length 118;
Best Local Similarity    100.0%; Pred. No. 4e-07;
Matches    20; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

```
Qy    1 INPETVPKPCCAPTQLNAIS 20
        ||||||||||||||||||||
Db   73 INPETVPKPCCAPTQLNAIS 92
```

RESULT 10
US-10-704-223-10
Sequence 10, Application US/10704223
Publication No. US20040152143A1
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY
APPLICANT: LEE, Se-Jin
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
FILE REFERENCE: JHU1190-7
CURRENT APPLICATION NUMBER: US/10/704,223
CURRENT FILING DATE: 2003-11-07
PRIOR APPLICATION NUMBER: US 10/115,406
PRIOR FILING DATE: 2002-04-02
PRIOR APPLICATION NUMBER: US 09/301,520
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: US 09/172,062
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: US 08/491,835
PRIOR FILING DATE: 1995-10-23
PRIOR APPLICATION NUMBER: PCT/US94/000685
PRIOR FILING DATE: 1994-01-12
PRIOR APPLICATION NUMBER: US 08/003,303
PRIOR FILING DATE: 1993-01-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
US-10-704-223-10
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Query Match   100.0%; Score 111; DB 16; Length 118;
Best Local Similarity   100.0%; Pred. No. 4e-07;
Matches   20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    1 INPETVPKPCCAPTQLNAIS 20
        ||||||||||||||||||||
Db   73 INPETVPKPCCAPTQLNAIS 92
```

RESULT 11
US-09-813-459-13
Sequence 13, Application US/09813459
Patent No. US20020107369A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: Cunningham, Noreen
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,459
FILING DATE: 20-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/624,635
FILING DATE: <Unknown>
```

ATTORNEY/AGENT INFORMATION:
  NAME: Wetherell, Jr., Ph.D., John R.,
  REGISTRATION NUMBER: 31,678
  REFERENCE/DOCKET NUMBER: PD-3054
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (619) 455-5100
    TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 13:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 119 amino acids
    TYPE: amino acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: protein
  IMMEDIATE SOURCE:
    CLONE: OP-1
  FEATURE:
    NAME/KEY: Protein
    LOCATION: 1..119
  SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-813-459-13

Qy    1 INPETVPKPCCAPTQLNAIS 20
        ||||||||||||||||||||
Db   74 INPETVPKPCCAPTQLNAIS 93

Query Match      100.0%;  Score 111;  DB 9;  Length 119;
Best Local Similarity  100.0%;  Pred. No. 4e-07;
Matches  20;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

RESULT 12
US-09-859-211-40
Sequence 40, Application US/09859211
Patent No. US2002015712S5A1
GENERAL INFORMATION:
  APPLICANT: Lee, Se-Jin
  APPLICANT: McPherron, Alexandra C.
  TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
  FILE REFERENCE: 07265/144001
  CURRENT APPLICATION NUMBER: US/09/859,211
  CURRENT FILING DATE: 2001-05-15
  PRIOR APPLICATION NUMBER: 09/019,070
  PRIOR FILING DATE: 1998-02-05
  PRIOR APPLICATION NUMBER: 08/862,445
  PRIOR FILING DATE: 1997-05-23
  PRIOR APPLICATION NUMBER: 08/847,910
  PRIOR FILING DATE: 1997-04-28
  PRIOR APPLICATION NUMBER: 08/795,071
  PRIOR FILING DATE: 1997-02-05
  PRIOR APPLICATION NUMBER: 08/525,596
  PRIOR FILING DATE: 1995-10-26
  PRIOR APPLICATION NUMBER: PCT/US94/03019
  PRIOR FILING DATE: 1994-03-18
  PRIOR APPLICATION NUMBER: 08/033,923
  PRIOR FILING DATE: 1993-03-19
  NUMBER OF SEQ ID NOS: 51
  SOFTWARE: FastSEQ for Windows Version 4.0
  SEQ ID NO 40
  LENGTH: 119
  TYPE: PRT
  ORGANISM: Homo sapiens

US-09-859-211-40

Qy    1 INPETVPKPCCAPTQLNAIS 20
        ||||||||||||||||||||
Db   74 INPETVPKPCCAPTQLNAIS 93

---

RESULT 13
US-09-880-708-18
Sequence 18, Application US/09880708
Patent No. US2002016536IA1
GENERAL INFORMATION:
  APPLICANT: Lee, Se-Jin
    Huynh, Thanh
  TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
  NUMBER OF SEQUENCES: 28
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Gray Cary Ware & Freidenrich LLP
    STREET: 4365 Executive Drive, Suite 1600
    CITY: San Diego
    STATE: CA
    COUNTRY: USA
    ZIP: 92121-2189
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette
    COMPUTER: IBM Compatible
    OPERATING SYSTEM: Windows95
    SOFTWARE: FastSEQ for Windows Version 2.0
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/880,708
    FILING DATE: 12-Jun-2001
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 09/145,060
    FILING DATE: <Unknown>
    APPLICATION NUMBER: 08/003,144
    FILING DATE: 12-JAN-1993
  ATTORNEY/AGENT INFORMATION:
    NAME: Lisa A. Haile, Ph.D.
    REGISTRATION NUMBER: 38,347
    REFERENCE/DOCKET NUMBER: 07265/057002
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 858/677-1456
    TELEFAX: 619/677-1465
  INFORMATION FOR SEQ ID NO: 18:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 119 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
    MOLECULE TYPE: protein
    IMMEDIATE SOURCE:
      CLONE: OP-1
    SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-09-880-708-18

Qy    1 INPETVPKPCCAPTQLNAIS 20
        ||||||||||||||||||||
Db   74 INPETVPKPCCAPTQLNAIS 93

Query Match      100.0%;  Score 111;  DB 9;  Length 119;
Best Local Similarity  100.0%;  Pred. No. 4e-07;
Matches  20;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

RESULT 14
US-09-872-856-40
Sequence 40, Application US/09872856
Publication No. US20030074680A1
GENERAL INFORMATION:
  APPLICANT: Johns Hopkins University School of Medicine
  APPLICANT: Lee, Se-Jin
  APPLICANT: McPherron, Alexandra
  TITLE OF INVENTION: Growth Differentiation Factor-8
  FILE REFERENCE: JHU1120-17
  CURRENT APPLICATION NUMBER: US/09/872,856
  CURRENT FILING DATE: 2001-06-01
  PRIOR APPLICATION NUMBER: US 09/124,180
  PRIOR FILING DATE: 1998-07-28
  PRIOR APPLICATION NUMBER: US 09/019,070
  PRIOR FILING DATE: 1998-02-05
  PRIOR APPLICATION NUMBER: US 08/862,445

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;     PRIOR FILING DATE: 1997-05-23
;     PRIOR APPLICATION NUMBER: US 08/847,910
;     PRIOR FILING DATE: 1997-04-28
;     PRIOR APPLICATION NUMBER: US 08/795,071
;     PRIOR FILING DATE: 1997-02-05
;     PRIOR APPLICATION NUMBER: US 08/525,596
;     PRIOR FILING DATE: 1995-10-25
;     PRIOR APPLICATION NUMBER: PCT/US 94/03019
;     PRIOR FILING DATE: 1994-03-18
;     PRIOR APPLICATION NUMBER: US 08/033,923
;     PRIOR FILING DATE: 1993-03-19
;     NUMBER OF SEQ ID NOS: 53
;     SOFTWARE: PatentIn version 3.1
;
;     SEQ ID NO 40
;     LENGTH: 119
;     TYPE: PRT
;     ORGANISM: Homo sapiens
US-09-872-856-40

Qy            1    INPETVPKPCCAPTQLNAIS 20
                   ||||||||||||||||||||
Db           74    INPETVPKPCCAPTQLNAIS 93

Query Match            100.0%;  Score 111;  DB 10;  Length 119;
Best Local Similarity  100.0%;  Pred. No. 4e-07;
Matches 20;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

RESULT 15
US-10-463-973-40
Sequence 40, Application US/10463973
Publication No. US20040055027A1
GENERAL INFORMATION:
   APPLICANT: Johns Hopkins University School of Medicine
   APPLICANT:      Lee, Se-Jin
   APPLICANT:      McPherron, Alexandra
   TITLE OF INVENTION: Growth Differentiation Factor-8
   FILE REFERENCE: JHU1120-17
   CURRENT APPLICATION NUMBER: US/10/463,973
   CURRENT FILING DATE:  2003-06-17
   PRIOR APPLICATION NUMBER: US/09/872,856
   PRIOR FILING DATE: 2001-06-01
   PRIOR APPLICATION NUMBER: US 09/124,180
   PRIOR FILING DATE: 1998-07-28
   PRIOR APPLICATION NUMBER: US 09/019,070
   PRIOR FILING DATE: 1998-02-05
   PRIOR APPLICATION NUMBER: US 08/862,445
   PRIOR FILING DATE: 1997-05-23
   PRIOR APPLICATION NUMBER: US 08/847,910
   PRIOR FILING DATE: 1997-04-28
   PRIOR APPLICATION NUMBER: US 08/795,071
   PRIOR FILING DATE: 1997-02-05
   PRIOR APPLICATION NUMBER: US 08/525,596
   PRIOR FILING DATE: 1995-10-25
   PRIOR APPLICATION NUMBER: PCT/US 94/03019
   PRIOR FILING DATE: 1994-03-18
   PRIOR APPLICATION NUMBER: US 08/033,923
   PRIOR FILING DATE: 1993-03-19
   NUMBER OF SEQ ID NOS: 53
   SOFTWARE: PatentIn version 3.1

   SEQ ID NO 40
   LENGTH: 119
   TYPE: PRT
   ORGANISM: Homo sapiens
US-10-463-973-40

Qy            1    INPETVPKPCCAPTQLNAIS 20
                   ||||||||||||||||||||
Db           74    INPETVPKPCCAPTQLNAIS 93

Query Match            100.0%;  Score 111;  DB 12;  Length 119;
Best Local Similarity  100.0%;  Pred. No. 4e-07;
Matches 20;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: October 12, 2004, 09:10:03 ; Search time 30 Seconds
            (without alignments)
            64.128 Million cell updates/sec

Title: US-10-619-910-11
Perfect score: 111
Sequence: 1 INPETVPKPCCAPTQLNAIS 20

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR.78:*
        1:    pir1:*
        2:    pir2:*
        3:    pir3:*
        4:    pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	111	100.0	313	2	I51284	bone morphogenetic
2	111	100.0	431	2	BMHU7	bone morphogenetic
3	108	97.3	430	2	JQ1184	osteogenic protein
4	107	96.4	426	2	JH0690	bone morphogenetic
5	97	87.4	207	2	S37618	vgr protein - rat
6	97	87.4	510	2	A54798	Vg-1-related prote
7	97	87.4	513	1	BMHU6	bone morphogenetic
8	87	78.4	452	2	I49542	bone morphogenetic
9	87	78.4	454	1	BMHU5	bone morphogenetic
10	84	75.7	34	2	A36626	osteogenic protein
11	77	69.4	455	2	A43918	TGF-beta-related p
12	71	64.0	360	2	A29619	Vg1 embryonic grow
13	71	64.0	588	2	A24158	decapentaplegic pr
14	70	63.1	402	2	A45056	osteogenic protein
15	70	63.1	461	2	S25408	SPDVR1 protein - s
16	64	57.7	365	2	T42286	cet-1 protein - Ca
17	64	57.7	400	2	A49147	bone morphogenetic
18	64	57.7	401	2	JH0689	bone morphogenetic
19	64	57.7	405	2	IS0608	bone morphogenetic
20	64	57.7	408	1	BMHU4	bone morphogenetic
21	64	57.7	408	2	JH0801	bone morphogenetic
22	64	57.7	408	2	S38343	bone morphogenetic
23	64	57.7	408	2	S58791	bone morphogenetic
24	64	57.7	408	2	S10529	bone morphogenetic
25	64	57.7	427	2	I49541	bone morphogenetic
26	63	56.8	309	2	A40735	TGF beta homolog d
27	63	56.8	309	2	JC5697	placental transfor
28	63	56.8	353	2	IS0607	bone morphogenetic
29	63	56.8	393	2	S37073	bone morphogenetic
30	63	56.8	394	2	S45355	bone morphogenetic
30	63	56.8	396	1	BMHU2	bone morphogenetic
31	63	56.8	398	2	JH0688	bone morphogenetic
32	63	56.8	398	2	JH0687	bone morphogenetic
33	63	56.8	495	2	S43294	bone morphogenetic
34	63	56.8	501	2	A55452	cartilage-derived
35	63	56.8	501	2	JC2347	growth/differentia
36	55	49.5	125	2	S43295	bone morphogenetic
37	55	49.5	436	2	B55452	cartilage-derived
38	54	48.6	409	2	S01825	transforming growt
39	54	48.6	409	2	A41397	transforming growt
40	54	48.6	410	2	A55706	transforming growt
41	54	48.6	412	2	A36169	transforming growt
42	54	48.6	412	2	A34939	transforming growt
43	54	48.6	413	2	JC4862	activin beta-A cha
44	54	48.6	476	2	JC4646	activin beta-A cha
45	54	48.6	478	2	JC4838	bone morphogenetic

ALIGNMENTS

RESULT 1
I51284
bone morphogenetic protein-7 - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 16-Jul-1999
C;Accession: I51284
J;Houston, B.; Thorp, B.H.; Burt, D.W.
J. Mol. Endocrinol. 13, 289-301, 1994
A;Title: Molecular cloning and expression of bone morphogenetic protein-7 in the chick e
R;Houston, B.; Thorp, B.H.; Burt, D.W.
A;Accession: I51284
A;Reference number: I51284; MUID:95200473; PMID:7893347
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-313 <HOU>
A;Cross-references: GB:S77477; NID:g957233; PIDN:AAB33846.1; PID:g957234
C;Superfamily: inhibin

Qy					
Db	268	INPETVPKPCCAPTQLNAIS 287			

Query Match   100.0%; Score 111; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 9.7e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 INPETVPKPCCAPTQLNAIS 20
             ||||||||||||||||||||
Db   268 INPETVPKPCCAPTQLNAIS 287

RESULT 2
BMHU7
bone morphogenetic protein 7 precursor - human
N;Alternate names: osteogenic protein 1
C;Species: Homo sapiens (man)
C;Date: 18-Oct-1991 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
C;Accession: C39263; S10529
R;Celeste, A.J.; Iannazzi, J.A.; Taylor, R.C.; Hewick, R.M.; Rosen, V.; Wang, E.A.; Wozn
Proc. Natl. Acad. Sci. U.S.A. 87, 9843-9847, 1990
R;Oezkaynak, E.; Rueger, D.C.; Drier, E.A.; Corbett, C.; Ridge, R.J.; Sampath, T.K.; Opp
EMBO J. 9, 2085-2093, 1990
A;Title: OP-1 cDNA encodes an osteogenic protein in the TGF-beta family.
A;Reference number: S10529; MUID:90291971; PMID:2357959
A;Accession: S10529
A;Molecule type: mRNA
A;Residues: 1-431 <OEZ>
A;Cross-references: EMBL:X51801; NID:g35151; PIDN:CAA36100.1; PID:g35152
C;Genetics:
A;Gene: GDB:BMP7
A;Cross-references: GDB:127597; OMIM:112267
A;Title: Identification of transforming growth factor beta family members present in bon
A;Reference number: A39263; MUID:91088608; PMID:2263636
A;Accession: C39263
A;Molecule type: mRNA
A;Residues: 1-431 <CEL>
A;Cross-references: GB:M60316; GB:M38695; NID:g339563; PIDN:AAA36738.1; PID:g339564

A;Map position: 20pter-20qter
C;Superfamily: inhibin
C;Keywords: bone; dimer; glycoprotein
F;1-29/Domain: signal sequence #status predicted <STG>
F;30-299/Domain: propeptide #status predicted <PRO>
F;300-431/Product: bone morphogenetic protein 7 #status predicted <MAT>
F;187,302,321,372/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match   100.0%; Score 111; DB 1; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 INPETVPKPCCAPTQLNAIS 20
       ||||||||||||||||||||
Db   386 INPETVPKPCCAPTQLNAIS 405

RESULT 3
JQ1184
osteogenic protein 1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Keywords: bone; dimer; glycoprotein
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 06-Dec-1996
C;Accession: JQ1184; P00224
R;Oezkaynak, E.; Schnegelsberg, P.N.J.; Oppermann, H.
Biochem. Biophys. Res. Commun. 179, 116-123, 1991
A;Title: Murine osteogenic protein (OP-1): high levels of mRNA in kidney.
A;Reference number: JQ1184; MUID:91354237; PMID:1715687
A;Molecule type: DNA
A;Residues: 1-120 <OE2>
A;Cross-references: EMBL:X56906
A;Accession: PQ0224
A;Molecule type: mRNA
A;Residues: 54-430 <OE2>
A;Accession: PQ0224
C;Superfamily: inhibin
C;Keywords: glycoprotein
C;Comment: This protein induces bone formation.

Query Match   97.3%; Score 108; DB 2; Length 430;
Best Local Similarity 95.0%; Pred. No. 3.6e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy   1 INPETVPKPCCAPTQLNAIS 20
       ||||||||||||:|||||||
Db   385 INPETVPKPCCAPTQLNAIS 404

RESULT 4
JH0690
bone morphogenetic protein 7 precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C;Accession: JH0690
R;Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.
Biochem. Biophys. Res. Commun. 186, 1487-1495, 1992
A;Title: Genes for bone morphogenetic proteins are differentially transcribed in early a
A;Reference number: JH0690; MUID:92378616; PMID:1510675
A;Molecule type: mRNA
A;Accession: JH0690
A;Residues: 1-426 <NIS>
A;Experimental source: oocyte
C;Superfamily: inhibin
C;Keywords: glycoprotein
F;283-426/Product: bone morphogenetic protein 7 #status predicted <MAT>
F;177,307,367/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match   96.4%; Score 107; DB 2; Length 426;
Best Local Similarity 95.0%; Pred. No. 4.9e-08;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   1 INPETVPKPCCAPTQLNAIS 20
       ||||||||||||||||||:||
Db   381 INPETVPKPCCAPTQLNGIS 400

RESULT 5
S37618
vgr protein - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Feb-1994 #text_change 26-May-1995 #text_change 16-Jul-1999
C;Accession: S37618
R;Sauermann, U.; Meyermann, R.; Schluesener, H.J.
J. Neurosci. Res. 33, 142-147, 1992
A;Title: Cloning of a novel TGF-beta related cytokine, the vgr, from rat brain: cloning o
A;Reference number: S37618; MUID:93085758; PMID:1453478
A;Accession: S37618
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-207 <SAU>
A;Cross-references: EMBL:X58830; NID:g57475; PIDN:CAA41634.1; PID:g57476
A;Note: the sequence from Fig. 4 is inconsistent with that from Fig. 1 in having 88-Ser o
C;Superfamily: inhibin

Query Match   87.4%; Score 97; DB 2; Length 207;
Best Local Similarity 85.0%; Pred. No. 7.3e-07;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy   1 INPETVPKPCCAPTQLNAIS 20
       ||| ||||||||||:|||||
Db   162 MNPEYVPKPCCAPTKLNAIS 181

RESULT 6
A54798
Vg-1-related protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 16-Jul-1999
C;Accession: A54798; A33925; S47442
R;Gitelman, S.E.; Kobrin, M.S.; Ye, J.Q.; Lopez, A.R.; Lee, A.; Derynck, R.
J. Cell Biol. 126, 1595-1609, 1994
A;Title: Recombinant vgr-1/BMP-6-expressing tumors induce fibrosis and endochondral bone
A;Reference number: A54798; MUID:94375533; PMID:8089189
A;Accession: A54798
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-510 <GIT>
A;Cross-references: EMBL:X80992; NID:g530729; PIDN:CAA56917.1; PID:g530730
R;Lyons, K.; Graycar, J.L.; Lee, A.; Hashmi, S.; Lindquist, P.B.; Chen, E.Y.; Hogan, B.L
Proc. Natl. Acad. Sci. U.S.A. 86, 4554-4558, 1989
A;Title: Vgr-1, a mammalian gene related to Xenopus Vg-1, is a member of the transformin
A;Reference number: A33925; MUID:89282810; PMID:2734307
A;Accession: A33925
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 'M',74,'K',76-85,'P',87-510 <LYO>
A;Cross-references: GB:J04566; NID:g202252; PIDN:AAA40548.1; PID:g202353
C;Superfamily: inhibin

Query Match   87.4%; Score 97; DB 2; Length 510;
Best Local Similarity 85.0%; Pred. No. 1.7e-06;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy   1 INPETVPKPCCAPTQLNAIS 20
       ||| ||||||||||:|||||
Db   465 MNPEYVPKPCCAPTKLNAIS 484

RESULT 7
BMHU6
bone morphogenetic protein 6 precursor - human
C;Species: Homo sapiens (man)

```
C;Date: 18-Oct-1991 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
R;Celeste, A.J.; Iannazzi, J.A.; Taylor, R.C.; Hewick, R.M.; Rosen, V.; Wang, E.A.; Wozn
Proc. Natl. Acad. Sci. U.S.A. 87, 9843-9847, 1990
A;Title: Identification of transforming growth factor beta family members present in bon
A;Reference number: B39263
A;Accession: B39263; MUID:91088608; PMID:2263636
A;Molecule type: mRNA
A;Residues: 1-513 <RES>
A;Cross-references: GB:M60315; GB:M38694; NID:g339561; PIDN:AAA36737.1; PID:g339562
C;Genetics:
A;Gene: GDB:BMP6
C;Genetics:
A;Map position: 6pter-6qter
A;Superfamily: inhibin
C;Keywords: bone; glycoprotein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-374/Domain: propeptide #status predicted <PRO>
F;375-513/Product: bone morphogenetic protein 6 #status predicted <MAT>
F;241,269,386,404,454/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match           87.4%;  Score 97;  DB 1;  Length 513;
Best Local Similarity  85.0%;  Pred. No. 1.7e-06;
Matches  17;  Conservative  2;  Mismatches  1;  Indels  0;  Gaps  0;

Qy    1 INPETVPKPCCAPTQLNAIS 20
          ||||||||||||||||||
Db  468 MNPEYVPKPCCAPTKLNAIS 487


RESULT 8
I49542
bone morphogenetic protein 5 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C;Accession: I49542
R;King, J.A.; Marker, P.C.; Seung, K.J.; Kingsley, D.M.
Dev. Biol. 166, 112-122, 1994
A;Title: BMP5 and the molecular, skeletal, and soft-tissue alterations in short ear mice
A;Reference number: I49542; MUID:95046894; PMID:7958439
A;Accession: I49542
A;Molecule type: mRNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-452 <RES>
C;Genetics:
A;Gene: GB:L41145; NID:g755033; PIDN:AAA64612.1; PID:g755034
C;Genetics:
A;Gene: BMP5
C;Superfamily: inhibin

Query Match           78.4%;  Score 87;  DB 2;  Length 452;
Best Local Similarity  83.3%;  Pred. No. 4.2e-05;
Matches  15;  Conservative  2;  Mismatches  1;  Indels  0;  Gaps  0;

Qy    3 PETVPKPCCAPTQLNAIS 20
          |:||||||||||||||||
Db  409 PDHVPKPCCAPTKLNAIS 426


RESULT 9
BMHU5
bone morphogenetic protein 5 precursor - human
C;Species: Homo sapiens (man)
C;Date: 18-Oct-1991 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
C;Accession: A39263
R;Celeste, A.J.; Iannazzi, J.A.; Taylor, R.C.; Hewick, R.M.; Rosen, V.; Wang, E.A.; Wozn
Proc. Natl. Acad. Sci. U.S.A. 87, 9843-9847, 1990
A;Title: Identification of transforming growth factor beta family members present in bon
A;Reference number: A39263; MUID:91088608; PMID:2263636
A;Accession: A39263
A;Molecule type: mRNA
A;Residues: 1-454 <CEL>
A;Cross-references: GB:M38693; GB:M60314; NID:g339559; PIDN:AAA36736.1; PID:g339560
C;Genetics:
A;Gene: GDB:BMP5
C;Cross-references: GDB:127595; OMIM:112265
A;Map position: 6pter-6qter
C;Superfamily: inhibin
C;Keywords: bone; glycoprotein
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-316/Domain: propeptide #status predicted <PRO>
F;317-454/Product: bone morphogenetic protein 5 #status predicted <MAT>
F;211,327,345,395/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match           78.4%;  Score 87;  DB 1;  Length 454;
Best Local Similarity  83.3%;  Pred. No. 4.3e-05;
Matches  15;  Conservative  2;  Mismatches  1;  Indels  0;  Gaps  0;

Qy    3 PETVPKPCCAPTQLNAIS 20
          |:||||||||||||||||
Db  411 PDHVPKPCCAPTKLNAIS 428


RESULT 10
A36626
osteogenic protein 18K chain - bovine (fragments)
C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 03-May-1996
C;Accession: A36626
R;Sampath, T.K.; Coughlin, J.E.; Whetstone, R.M.; Banach, D.; Corbett, C.; Ridge, R.J.;
J. Biol. Chem. 265, 13198-13205, 1990
A;Title: Bovine osteogenic protein is composed of dimers of OP-1 and BMP-2A, two members
A;Reference number: A36626; MUID:90330665; PMID:2376592
A;Accession: A36626
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-34 <SAM>
A;Superfamily: inhibin

Query Match           75.7%;  Score 84;  DB 2;  Length 34;
Best Local Similarity  100.0%;  Pred. No. 1.1e-05;
Matches  14;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 INPETVPKPCCAPT 14
          ||||||||||||||
Db   21 INPETVPKPCCAPT 34


RESULT 11
A43918
TGF-beta-related protein 60A precursor - fruit fly (Drosophila melanogaster)
N;Alternate names: bone morphogenetic protein homolog precursor
C;Species: Drosophila melanogaster
C;Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C;Accession: A43918; A41233
R;Wharton, K.A.; Thomsen, G.H.; Gelbart, W.M.
Proc. Natl. Acad. Sci. U.S.A. 88, 9214-9218, 1991
A;Title: Drosophila 60A gene, another transforming growth factor beta family member, is c
A;Reference number: A41233; MUID:92201021; PMID:1924384
R;Doctor, J.S.; Jackson, P.D.; Rashka, K.E.; Visalli, M.; Hoffmann, F.M.
Dev. Biol. 151, 491-505, 1992
A;Title: Sequence, biochemical characterization, and developmental expression of a new m
A;Reference number: A43918; MUID:92290120; PMID:160181
A;Accession: A43918
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-455 <DOC>
A;Cross-references: GB:M84795; NID:g156729; PIDN:AAA28307.1; PID:g156730
N;Note: sequence extracted from NCBI backbone (NCBIN:106399, NCBIP:106400)
A;Cross-references: GB:M77012; NID:g156727; PIDN:AAA28306.1; PID:g156728
A;Residues: 1-455 <WHA>
C;Genetics:
A;Gene: 60A
C;Comment: This protein is a member of the transforming growth factor beta family.
C;Genetics:
A;Gene: 60A
A;Cross-references: FlyBase:FBgn0024234
```

C;Superfamily: inhibin
C;Keywords: homodimer

Qy   1 INPETVPKPCCAPTQLNAI 19
Query Match ||||||||||||
Best Local Similarity   69.4%;   Score 77;   DB 2;   Length 455;
Matches 12;   Conservative 4;   Mismatches 3;   Indels 0;   Gaps 0;

Db   410 LEPKKVPKPCCAPTRLGAL 428

RESULT 12
A29619
Vg1 embryonic growth factor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989
C;Accession: A29619
R;Weeks, D.L.; Melton, D.A.
Cell 51, 861-867, 1987
A;Title: A maternal mRNA localized to the vegetal hemisphere in Xenopus eggs codes for a
A;Reference number: A29619; MUID:88052889; PMID:3479264
A;Cross-references: GB:M18055; NID:g214179; PIDN:AAA49727.1; PID:g214180
A;Superfamily: inhibin
A;Molecule type: mRNA
A;Residues: 1-360 <WEE>
A;Accession: A29619
C;Superfamily: inhibin
C;Keywords: growth factor

Qy   1 INPETVPKPCCAPTQLNAIS 20
Query Match ||||||||||||
Best Local Similarity   64.0%;   Score 71;   DB 2;   Length 360;
Matches 11;   Conservative 4;   Mismatches 5;   Indels 0;   Gaps 0;

Db   315 IEPEDIPLPCCVPTKMSPIS 334

RESULT 13
A26158
decapentaplegic protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 24-Jun-1987 #sequence_revision 24-Jun-1987 #text_change 16-Apr-1999
C;Accession: A26158
R;Padgett, R.W.; St. Johnston, R.D.; Gelbart, W.M.
Nature 325, 81-84, 1987
A;Title: A transcript from a Drosophila pattern gene predicts a protein homologous to th
A;Reference number: A26158; MUID:87050408; PMID:3467201
A;Accession: A26158
A;Molecule type: mRNA
A;Residues: 1-588 <PAD>
A;Cross-references: GB:M30116; NID:g157291; PID:g157292
C;Genetics:
A;Gene: FlyBase:dpp
A;Cross-references: FlyBase:FBgn0000490
C;Keywords: glycoprotein
F;1-15/Domain: signal sequence #status predicted <SIG>
F;120,342,377,529/Binding site: carbohydrate (Asn) (covalent) #status predicted

Qy   1 INPETVPKPCCAPTQLNAIS 20
Query Match ||||||||||||
Best Local Similarity   64.0%;   Score 71;   DB 2;   Length 588;
Matches 11;   Conservative 5;   Mismatches 4;   Indels 0;   Gaps 0;

Db   543 MNPGKVPKACCVPTQLDSVA 562

RESULT 14
A45056
osteogenic protein 2 precursor - human
N;Alternate names: bone morphogenetic protein 8; OP-2
C;Species: Homo sapiens (man)
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C;Accession: A45056
R;Oezkaynak, E.; Schnegelsberg, P.N.; Jin, D.F.; Clifford, G.M.; Warren, F.D.; Drier, E.A
J. Biol. Chem. 267, 25220-25227, 1992
A;Title: Osteogenic protein-2. A new member of the transforming growth factor-beta super
A;Reference number: A45056; MUID:93094231; PMID:1460021
A;Accession: A45056
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-402 <OZK>
A;Cross-references: hippocampus
A;Note: sequence extracted from NCBI backbone (NCBIP:120189)
C;Genetics:
A;Gene: GDB:BMP8; OP-2
A;Cross-references: GDB:136392
A;Superfamily: inhibin

Qy   1 INPETVPKPCCAPTQLNAIS 20
Query Match ||||||||||||
Best Local Similarity   63.1%;   Score 70;   DB 2;   Length 402;
Matches 12;   Conservative 3;   Mismatches 5;   Indels 0;   Gaps 0;

Db   357 MKPNAVPKACCAPTKLSATS 376

RESULT 15
S52408
SPDVR1 protein - sea urchin (Strongylocentrotus purpuratus)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 20-Sep-1999
C;Accession: S52408
R;Ponce, M.R.; Micol, J.L.; Davidson, E.H.
submitted to the EMBL Data Library, February 1995
A;Description: SpDVR1, a member of the transforming growth factor-beta superfamily expres
A;Reference number: S52408
A;Accession: S52408
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-461 <PON>
A;Cross-references: EMBL:Z48313; NID:g673496; PID:g673497
C;Superfamily: inhibin

Qy   1 INPETVPKPCCAPTQLNAIS 20
Query Match ||||||||||||
Best Local Similarity   63.1%;   Score 70;   DB 2;   Length 461;
Matches 11;   Conservative 6;   Mismatches 3;   Indels 0;   Gaps 0;

Db   416 MSPSHVPQPCCAPTKLSPIT 435

Search completed: October 12, 2004, 09:38:16
Job time : 31 secs

OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: October 12, 2004, 09:02:13

Title: US-10-619-910-11
Perfect score: 111
Sequence: 1 INPETVPKPCCAPTQLNAIS 20

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database :

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          SPTREMBL_25:*
      1:  sp_archea:*
      2:  sp_bacteria:*
      3:  sp_fungi:*
      4:  sp_human:*
      5:  sp_invertebrate:*
      6:  sp_mammal:*
      7:  sp_mhc:*
      8:  sp_organelle:*
      9:  sp_phage:*
     10:  sp_plant:*
     11:  sp_rodent:*
     12:  sp_virus:*
     13:  sp_vertebrate:*
     14:  sp_unclassified:*
     15:  sp_rvirus:*
     16:  sp_bacteriap:*
     17:  sp_archeap:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Search time 89 Seconds
(without alignments)
70.903 Million cell updates/sec

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	111	100.0	49	6	Q9MZL9	Q9mzl9 canis famil
2	111	100.0	108	6	Q8MJC0	Q8mjc0 ovis aries
3	111	100.0	313	13	Q91403	Q91403 gallus gall
4	111	100.0	398	13	Q918T6	Q918t6 gallus gall
5	108	97.3	141	11	O88684	O88684 rattus norv
6	108	97.3	306	11	Q9R228	Q9r228 rattus norv
7	108	97.3	424	13	Q9GH7	Q9gh7 xenopus lae
8	102	91.9	432	13	Q9PTF9	Q9ptf9 brachydanio
9	100	91.9	100	6	Q8MJC1	Q8mjc1 ovis aries
10	97	87.4	435	11	Q8BRW3	Q8brw3 mus musculu
11	97	87.4	506	11	Q81S4	Q81s4 rattus norv
12	89	80.2	446	13	Q7t288	Q7t288 brachydanio
13	87	78.4	453	13	P87373	P87373 gallus gall
14	87	78.4	454	11	Q8CCE0	Q8cce0 mus musculu
15	79	71.2	87	5	Q9U1G4	Q9u1g4 haliotis tu
16	79	71.2	178	5	Q25211	Q25211 junonia coe

RESULT 1
Q9MZL9

ID Q9MZL9 PRELIMINARY; PRT; 49 AA.
AC Q9MZL9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Bone morphogenetic protein BMP7 (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Johanson J.A., Breen M., Murphy K.E.;
RT "Chromosomal Localization of the Genes Encoding Canine Bone
RT Morphogenetic Proteins 4 and 7 (BMP4 and BMP7).";
RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF172412; AAF89752.1; -.
DR HSSP; P18075; 1BMP.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF-beta; 1.
DR ProDom; PD003517; TGFb; 1.
DR SMART; SM00204; TGFB; 1.
FT NON_TER 1
SQ SEQUENCE 49 AA; 5493 MW; 9AF2C1B144E26EFB CRC64;

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Query Match             100.0%;  Score 111;  DB 6;  Length 49;
Best Local Similarity   100.0%;
Matches   20;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy          1 INPETVPKPCCAPTQLNAIS 20
              ||||||||||||||||||||
Db          1 INPETVPKPCCAPTQLNAIS 20
```

RESULT 2
Q8MJC0

ALIGNMENTS

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 17  78  70.3   204  5  Q9xz69  Q9xz69 tripneustes
 18  78  70.3   289  5  Q9xyQ8  Q9xyQ8 strongyloce
 19  78  70.3   417  5  Q9xyQ7  Q9xyq7 lytechinus
 20  78  69.4   461  5  Q8mxz3  Q8mxz3 hemicentrot
 21  77  69.4    85  5  Q8wr85  Q8wr85 antedon bif
 22  77  69.4    77  5  Q8WR85  Q8wr85 antedon bif
 23  76  68.5   301  5  O97390  O97390 crassostrea
 24  75  67.6   128  5  Q95W38  Q95w38 schistocerc
 25  74  66.7   354  13 Q9YGV1  Q9ygv1 xenopus lae
 26  74  66.7   614  5  P91720  P91720 drosophila
 27  73  65.8   191  5  Q26468  Q26468 schistocerc
 28  72  64.9   412  11 Q80VZ0  Q80vz0 mus musculu
 29  72  64.9   438  5  Q9GT26  Q9gt26 anopheles s
 30  71  64.0   356  13 Q7t2G5  Q7t2g5 xenopus bor
 31  71  64.0   399  11 Q8BNM2  Q8bnm2 mus musculu
 32  71  64.0   588  5  Q9VCC6  Q9vcc6 drosophila
 33  70  63.1   361  5  Q96504  Q96504 branchiosto
 34  70  63.1   378  5  Q8MXC2  Q8mxc2 acropora mi
 35  70  63.1   402  4  Q7zSY6  Q7zsy6 homo sapien
 36  70  63.1   411  5  Q9U418  Q9u418 branchiosto
 37  68.5 61.7  443  5  O76851  O76851 halocynthia
 38  68  61.3   398  13 Q9DYD7  Q9dyd7 xenopus tro
 39  68  61.3   370  5  Q969A4  Q969a4 achaearanea
 40  68  60.4   407  5  Q8MWG4  Q8mwg4 patella vul
 41  67  60.4   509  5  Q8WS99  Q8ws99 archaster t
 42  66  59.5    85  5  Q8BHM7  Q8bhm7 paracentrot
 43  66  59.5   301  5  Q6RL7   Q6rl7 ilyanassa o
 44  66  59.5   373  13 Q98950  Q98950 gallus gall
 45  65  58.6   373  13 Q90723  Q90723 gallus gall
 45  65  58.6    83  13 P79707  P79707 cynops pyrr
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ID   Q8MJC0      PRELIMINARY;   PRT;   108 AA.
AC   Q8MJC0;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Bone morphogenetic protein 7 (Fragment).
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Souza C.J.H., Baird D.T.;
RT   "BMP expression in the sheep ovary.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR   EMBL; AF508311; AAM46923.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR002405; Inhibin_alpha.
DR   InterPro; IPR001839; TGFb.
DR   Pfam; PF00019; TGF-beta; 1.
DR   PRINTS; PR00669; INHIBINA.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFb; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  12198 MW;  88516813EA521377 CRC64;

Qy          1 INPETVPKPCCAPTQLNAIS 20
              ||||||||||||||||||||
Db         85 INPETVPKPCCAPTQLNAIS 104

Query Match             100.0%;  Score 111;  DB 6;  Length 108;
Best Local Similarity   100.0%;  Pred. No. 2.2e-10;
Matches   20;  Conservative    0;  Mismatches   0;  Indels    0;  Gaps    0;

RESULT 3
ID   Q91403      PRELIMINARY;   PRT;   313 AA.
AC   Q91403;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Bone morphogenetic protein-7 (Fragment).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95200473; PubMed=7893347;
RA   Houston B., Thorp B.H., Burt D.W.;
RT   "Molecular cloning and expression of bone morphogenetic protein-7 in
RT   the chick epiphyseal growth plate.";
RL   J. Mol. Endocrinol. 13:289-301(1994).
CC   -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR   EMBL; S77477; AAB33846.1; -.
DR   PIR; I51284; I51284.
DR   HSSP; P18075; 1BMP.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR002405; Inhibin_alpha.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   PRINTS; PR00669; INHIBINA.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFb; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   313 AA;  35816 MW;  C0A3739197DBAC8F CRC64;

Qy          1 INPETVPKPCCAPTQLNAIS 20
              ||||||||||||||||||||
Db        268 INPETVPKPCCAPTQLNAIS 287

Query Match             100.0%;  Score 111;  DB 13;  Length 313;
Best Local Similarity   100.0%;  Pred. No. 6.3e-10;
Matches   20;  Conservative    0;  Mismatches   0;  Indels    0;  Gaps    0;

RESULT 4
ID   Q91816      PRELIMINARY;   PRT;   398 AA.
AC   Q91816;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Bone morphogenetic protein 7 (Fragment).
GN   BMP7.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Oviduct;
RX   MEDLINE=20307867; PubMed=10848589;
RA   Monroe D.G., Jin D.F., Sanders M.M.;
RT   "Estrogen Opposes the Apoptotic Effects of Bone Morphogenetic Protein
RT   7 on Tissue Remodeling.";
RL   Mol. Cell. Biol. 20:4626-4634(2000).
CC   -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR   EMBL; AF205877; AAF34179.1; -.
DR   HSSP; P18075; 1BMP.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR002405; Inhibin_alpha.
DR   InterPro; IPR001839; TGFb.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   PRINTS; PR00669; INHIBINA.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFb; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   398 AA;  45459 MW;  9C3F625299DD0C37 CRC64;

Qy          1 INPETVPKPCCAPTQLNAIS 20
              ||||||||||||||||||||
Db        353 INPETVPKPCCAPTQLNAIS 372

Query Match             100.0%;  Score 111;  DB 13;  Length 398;
Best Local Similarity   100.0%;  Pred. No. 8e-10;
Matches   20;  Conservative    0;  Mismatches   0;  Indels    0;  Gaps    0;

RESULT 5
ID   O88684      PRELIMINARY;   PRT;   141 AA.
AC   O88684;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Bone morphogenetic protein-7 (Fragment).
OS   Rattus norvegicus (Rat).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar;
RX   MEDLINE=97107792; PubMed=8950518;
RA   Takahashi H., Ikeda T.;
RT   "Transcripts for two members of the transforming growth factor-beta
RT   superfamily BMP-3 and BMP-7 are expressed in developing rat embryos.";
RL   Dev. Dyn. 20::439-449(1996).
CC   -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR   EMBL; D29769; BAA31853.1; -.
HSSP; P18075; 1BMP.
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
GO   GO:0005576; C:extracellular; IEA.
GO   GO:0008151; P:cell growth and/or maintenance; IEA.
InterPro; IPR002405; P:Inhibin_alpha.
DR   Eukaryota; Metazoa; Chordata; TGFB;
DR   InterPro; IPR001839; TGFB.
Pfam; PF00019; TGF-beta; 1.
PRINTS; PR00669; INHIBINA.
PRINTS; PR00669; INHIBINA.
ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
NON_TER       1
NON_TER     141
SEQUENCE  141 AA;  15850 MW;  1A02FA2213F39812 CRC64;
          INPETVRKPCCAPTQLNAIS

Qy         1 INPETVRKPCCAPTQLNAIS  20
             ||||||||||||||||||||
Db       110 INPDTVRKPCCAPTQLNAIS 129
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Query Match     97.3%;    Score 108;  DB 11;   Length 141;
Best Local Similarity   95.0%;   Pred. No. 8.7e-10;
Matches   19;  Conservative  1; Mismatches   0;  Indels   0;  Gaps   0;
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RESULT 6
ID   Q9R228
AC   Q9R228;
DT   01-MAY-2000 (TrEMBLrel. 1, Created)
PRELIMINARY;    PRT;    306 AA.
DT   01-MAY-2000 (TrEMBLrel. 1, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Bone morphogenetic protein 7 precursor (fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=Kidney;
RX   MEDLINE=99170602; PubMed=10070161;
RA   Simon M., Maresh J.G., Harris S.E., Hernandez J.D., Arar M.,
RA   Olson M.S., Abboud H.E.;
RT   "Expression of bone morphogenetic protein 7 mRNA in normal and
RT   ischemic adult rat kidney.";
RL   Am. J. Physiol. 276:F382-F389(1999).
CC   -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR   EMBL; AF100787; AAD27804.1; -.
HSSP; P18075; 1BMP.
InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb_N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
NON_TER       306
NON_TER       306
SEQUENCE  306 AA;  34953 MW;  BB53FC5CE959E400 CRC64;
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Query Match     97.3%;    Score 108;  DB 11;   Length 306;
Best Local Similarity   95.0%;   Pred. No. 1.9e-09;
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Matches   19;  Conservative  1; Mismatches   0;  Indels   0;  Gaps   0;

Qy         1 INPETVRKPCCAPTQLNAIS  20
             ||||||||||||||||||||
Db       274 INPDTVRKPCCAPTQLNAIS 293
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RESULT 7
ID   Q9YGH7
AC   Q9YGH7;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
PRELIMINARY;    PRT;    424 AA.
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Osteogenic protein-1 homolog precursor (Hypothetical protein).
GN   XOP-1H.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wang S., Krinks M., Kleinwaks L., Zapalo P., Moos M. Jr.;
RL   Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22341132; PubMed=12454917;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Klein S., Strausberg R.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR   EMBL; U40034; AAD09399.1; -.
EMBL; BC055959; AAH55959.1; -.
HSSP; P18075; 1BMP.
InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb_N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
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DR   PROSITE; PS00250; TGF_BETA_1; 1.
KW   Hypothetical protein; Signal.
FT   SIGNAL        9     29
FT   CHAIN        286    424    OSTEOGENIC PROTEIN-1 HOMOLOG.
SQ   SEQUENCE     424 AA;   48917 MW;  C4638C7D3D0A1DB4 CRC64;

Qy           1 INPETVPKPCCAPTQLNAIS 20
               |||:||||||||||||||||
Db         379 INPDTVPKPCCAPTQLNAIS 398

Query Match   97.3%;  Score 108; DB 13; Length 424;
Best Local Similarity   95.0%;  Pred. No. 2.6e-09;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;


RESULT 8
Q9PTF9
ID   Q9PTF9          PRELIMINARY;    PRT;   432 AA.
AC   Q9PTF9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Bone morphogenetic protein 7.
GN   BMP7 OR BMP7.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=TL;
RA   Dick A., Hild M., Bauer H., Imai Y., Maifeld H., Schier A.F.,
RA   Talbot W.S., Bouwmeester T., Hammerschmidt M.;
RT   "Essential role of Bmp7 (snailhouse) and its prodomain in dorsoventral
RT   patterning of the zebrafish embryo.";
RL   Development 0:0-0(2000).
CC   -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR   EMBL; AF201379; AAF17558.1; -.
DR   PROSITE; PS00250; TGF_BETA_1; -.
SQ   SEQUENCE     432 AA;   48923 MW;  C982AF80E1652156 CRC64;

Qy           1 INPETVPKPCCAPTQLNAIS 20
               ||||||||||||||||::||
Db         387 INPETVPKPCCAPTQLHGIS 406

Query Match   91.9%;  Score 102; DB 13; Length 432;
Best Local Similarity   90.0%;  Pred. No. 2.6e-08;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;


RESULT 9
Q8MJC1
ID   Q8MJC1          PRELIMINARY;    PRT;   100 AA.
AC   Q8MJC1;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Bone morphogenetic protein 6 (Fragment).
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Souza C.J.H., Baird D.T.;
RT   "BMP expression in the sheep ovary.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR   EMBL; AF508310; AAM46922.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005615; C:extracellular; IEA.
DR   GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR   InterPro; IPR002405; Inhibin_alpha.
DR   InterPro; IPR001839; TGFb.
DR   Pfam; PF00019; TGF-beta; 1.
DR   PRINTS; PR00669; INHIBINA.
DR   ProDom; PD000357; Inhibin_alpha.
DR   SMART; SM00204; TGFb; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
FT   NON_TER       1
FT   NON_TER     100
SQ   SEQUENCE     100 AA;   11309 MW;  8C8B61551F356350 CRC64;

Qy           1 INPETVPKPCCAPTQLNAIS 20
               :|||:|||||||||:|||||
Db          67 MNPEYVPKPCCAPTKLNAIS 86

Query Match   87.4%;  Score 97; DB 6; Length 100;
Best Local Similarity   85.0%;  Pred. No. 3.8e-08;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;


RESULT 10
Q8BRW3
ID   Q8BRW3          PRELIMINARY;    PRT;   435 AA.
AC   Q8BRW3;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Bone morphogenetic protein 6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Aorta, and Vein;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium;
RA   The RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK041210; BAC30864.1; -.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFb; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
SQ   SEQUENCE     435 AA;   48438 MW;  E26CFE2180B20F76 CRC64;

Qy           1 INPETVPKPCCAPTQLNAIS 20
               :|||:|||||||||:|||||
Db         390 MNPEYVPKPCCAPTKLNAIS 409

Query Match   87.4%;  Score 97; DB 11; Length 435;
Best Local Similarity   85.0%;  Pred. No. 1.7e-07;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;


RESULT 11
Q81IS4
ID   Q81IS4          PRELIMINARY;    PRT;   506 AA.
AC   Q81IS4;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
```

DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Bone morphogenetic protein 6.
GN   BMP6.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague Dawley;
RA   Li H., Li J., Pittman D.D., Amalfitano A., Hankins G.R., Helm G.A.;
RT   "An Immunological Study of BMP6 Adenoviral Gene Therapy.";
RL   Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY184240; AAO25744.1; -.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
SQ   SEQUENCE 506 AA; 56222 MW; 703D077D7E944116C CRC64;

Query Match   87.4%; Score 97; DB 11; Length 506;
Best Local Similarity   85.0%;   Pred. No. 2e-07;
Matches   17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy   1 INPETVKPKPCCAPTQLNAIS 20
           || |||| |||||||| ||||
Db   461 MNPEYVPKPCCAPTKLNAIS 480

RESULT 12
Q7T288
ID   Q7T288   PRELIMINARY;   PRT;   446 AA.
AC   Q7T288;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
OC   BMP5.

Query Match   80.2%; Score 89; DB 13; Length 446;
Best Local Similarity   83.3%;   Pred. No. 3.5e-06;
Matches   15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy   3 PETVKPKPCCAPTQLNAIS 20
           |: ||||||||||| ||||
Db   403 PDNVPKPCCAPTKLNAIS 420

RESULT 13
P87373
ID   P87373   PRELIMINARY;   PRT;   453 AA.
AC   P87373;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Bone morphogenetic protein 5.
GN   BMP5.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97000882; PubMed=8815925;
RA   Oh S.H., Johnson R., Wu D.K.;
RT   "Differential expression of bone morphogenetic proteins in the
RT   developing vestibular and auditory sensory organs.";
RL   J. Neurosci. 16:6463-6475(1996).
CC   -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR   EMBL; S83278; AAB49514.1; -.
DR   HSSP; P18075; 1BMP.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
SQ   SEQUENCE 453 AA; 51628 MW; AB946FE878BF32B2 CRC64;

Query Match   78.4%; Score 87; DB 13; Length 453;
Best Local Similarity   83.3%;   Pred. No. 7.5e-06;
Matches   15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy   3 PETVKPKPCCAPTQLNAIS 20
           |: ||||||||||| ||||
Db   410 PDHVPKPCCAPTKLNAIS 427

RESULT 14
Q8CCE0
ID   Q8CCE0   PRELIMINARY;   PRT;   454 AA.
AC   Q8CCE0;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Bone morphogenetic protein 5.
GN   BMP5.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.

```
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57B1/6J; TISSUE=Lung;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium;
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK033362; BAC28247.1; -.
DR   MGD; MGI:88181; Bmp5.
DR   GO; GO:0007389; P:pattern specification; IMP.
DR   GO; GO:0001501; P:skeletal development; IMP.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
SQ   SEQUENCE   454 AA;  51727 MW;  722EA34FF25D63A0 CRC64;

Query Match             78.4%;  Score 87;  DB 11;  Length 454;
Best Local Similarity   83.3%;  Pred. No. 7.5e-06;
  Matches   15;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 PETVPKPCCAPTQLNAIS 20
                |:|||||||:||||||
Db        411 PDHVPKPCCAPTKLNAIS 428


RESULT 15
ID   Q9U1G4
AC   Q9U1G4;
ID   Q9U1G4      PRELIMINARY;      PRT;    87 AA.
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   BMP2/4 protein (Fragment).
GN   BMP2/4.
OS   Haliotis tuberculata.
OC   Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC   Vetigastropoda; Haliotoidea; Haliotidae; Haliotis.
OX   NCBI_TaxID=36103;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Mantle;
RX   MEDLINE=21261484; PubMed=11368850;
RA   Lelong C., Mathieu M., Favrel P.;
RT   "Identification of new bone morphogenetic protein-related members in
RT   invertebrates.";
RL   Biochimie 83:423-426(2001).
CC   -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR   EMBL; AJ251823; CAB63656.1; -.
DR   HSSP; P12643; 3BMP.
DR   InterPro; IPR001839; TGFb.
DR   Pfam; PF00019; TGF-beta; 1.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
FT   NON_TER       1      1
FT   NON_TER      87     87
SQ   SEQUENCE   87 AA;  9565 MW;  705965FCBCDBFFE6 CRC64;

Query Match             71.2%;  Score 79;  DB 5;  Length 87;
Best Local Similarity   65.0%;  Pred. No. 2.9e-05;
  Matches   13;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 INPETVPKPCCAPTQLNAIS 20
                :||   |||  ||:|||:|||
Db         44 VNPSAVPKACCVPTELTAIS 63
```

OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: October 12, 2004, 09:02:13 ; Search time 19 Seconds
(without alignments)
54.811 Million cell updates/sec

Title: US-10-619-910-11
Perfect score: 111
Sequence: 1 INPETVPKPCCAPTQLNAIS 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 141681

Searched: 141681 seqs, 52070155 residues

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	
1	111	100.0	431	1	P18075	homo sapien	BMP7_HUMAN
2	108	97.3	430	1	P23359	mus musculu	BMP7_MOUSE
3	107	96.4	426	1	P30886	xenopus lae	BMP7_XENLA
4	97	87.4	207	1	Q04906	rattus norv	BMP6_RAT
5	97	87.4	510	1	P20722	mus musculu	BMP6_MOUSE
6	97	87.4	513	1	P22004	homo sapien	BMP6_HUMAN
7	87	78.4	452	1	P49001	mus musculu	BMP5_MOUSE
8	87	78.4	454	1	P22003	homo sapien	BMP5_HUMAN
9	77	69.4	436	1	Q24735	drosophila	60A_DROVI
10	77	69.4	455	1	P27091	drosophila	60A_DROME
11	72	64.9	399	1	P34821	mus musculu	BM8A_MOUSE
12	72	64.9	621	1	P91699	drosophila	DECA_DROPS
13	71	64.0	360	1	P09534	xenopus lae	DVR1_XENLA
14	71	64.0	399	1	P55105	mus musculu	BM8B_MOUSE
15	71	64.0	588	1	P07713	drosophila	DECA_DROME
16	71	64.0	593	1	P91706	drosophila	DECA_DROSI
17	70	63.1	402	1	P34820	homo sapien	BM8B_HUMAN
18	70	63.1	461	1	P49969	homo sapien	DVR1_STRPU
19	67	60.4	372	1	Q26974	strongyloce	DVR1_STRPU
20	67	60.4	395	1	P48970	strongyloce	DECA_TRICA
21	65	58.6	401	1	P30885	xenopus lae	UNIV_STRPU
22	64	57.7	405	1	Q90752	gallus gall	BMP4_XENLA
23	64	57.7	408	1	Q29607	dama dama (	BMP4_CHICK
24	64	57.7	408	1	P12644	homo sapien	BMP4_DAMDA
25	64	57.7	408	1	P21275	mus musculu	BMP4_HUMAN
26	64	57.7	408	1	O08826	rattus norv	BMP4_MOUSE
27	64	57.7	409	1	P34822	gallus gall	BMP4_RAT
28	64	57.7	427	1	Q99988	homo sapien	BMP4_RABIT
29	63	56.8	308	1	Q90751	gallus gall	GDFF_HUMAN
30	63	56.8	308	1	O46576	oryctolagus	DSL1_CHICK
31	63	56.8	393	1	P49001	rattus norv	BMP2_CHICK
32	63	56.8	394	1	P21274	mus musculu	BMP2_RAT
33	63	56.8	395	1	O46564	oryctolagus	BMP2_MOUSE
34	63	56.8	396	1	O19006	dama dama (	BMP2_DAMDA
35	63	56.8	396	1	P12643	homo sapien	BMP2_HUMAN
36	63	56.8	398	1	P25703	xenopus lae	BMPA_XENLA
37	63	56.8	398	1	P30884	xenopus lae	BMPB_XENLA
38	63	56.8	495	1	P43027	mus musculu	GDF5_MOUSE
39	63	56.0	501	1	P43026	homo sapien	GDF5_HUMAN
40	61	55.0	400	1	P54631	drosophila	SCW_DROME
41	59	53.2	355	1	P35621	brachydanio	DVR1_BRARE
42	55	49.5	125	1	P43028	mus musculu	GDF6_MOUSE
43	55	49.5	436	1	P55106	bos taurus	GDF6_BOVIN
44	54	48.6	303	1	Q9Z0J7	mus musculu	GDF5_MOUSE
45	54	48.6	303	1	Q9Z0J6	rattus norv	GDF5_RAT

RESULT 1
BMP7_HUMAN

ALIGNMENTS

```
ID   BMP7_HUMAN     STANDARD;      PRT;   431 AA.
AC   P18075; Q99512; Q9NTQ7;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Bone morphogenetic protein 7 precursor (BMP-7) (Osteogenic protein 1)
DE   (OP-1).
GN   BMP7 OR OP1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   TISSUE=Placenta;
RX   MEDLINE=90291971; PubMed=2357959;
RA   Oezkaynak E., Rueger D.C., Drier E.A., Corbett C., Ridge R.J.,
RA   Sampath T.K., Opperman H.;
RT   "OP-1 cDNA encodes an osteogenic protein in the TGF-beta family.";
RL   EMBO J. 9:2085-2093(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91088608; PubMed=2263336;
RA   Celeste A.J., Iannazzi J.A., Taylor R.C., Hewick R.M., Rosen V.,
RA   Wang E.A., Wozney J.M.;
RT   "Identification of transforming growth factor beta family members
RT   present in bone-inductive protein purified from bovine bone.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:9843-9847(1990).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21638749; PubMed=11780052;
RA   Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA   Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA   Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA   Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA   Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA   Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA   Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA   Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA   Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA   Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA   Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA   Huckle E., Hunt S.E., Hunt A.R., Jekosch K., Johnson C.M., Johnson D.,
RA   Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA   Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA   Marsh V.L., Martin S., McConnachie L.J., McLay K., McMurray A.A.,
RA   Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA   Oliver K., Parker A., Patel R., Pearce A.V., Peck A.I.,
RA   Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA   Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA   Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA   Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA   Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA   Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
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RA   Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA   Rogers J.;
RT   "The DNA sequence and comparative analysis of human chromosome 20.";
RL   Nature 414:865-871(2001).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 293-431.
RX   MEDLINE=96149402; PubMed=8570652;
RA   Griffith D.L., Keck P.C., Sampath T.K., Rueger D.C., Carlson W.D.;
RT   "Three-dimensional structure of recombinant human osteogenic protein
RT   1: structural paradigm for the transforming growth factor beta
RT   superfamily.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:878-883(1996).
-!- FUNCTION: Induces cartilage and bone formation. May be the
CC   osteoinductive factor responsible for the phenomenon of epithelial
CC   osteogenesis. Plays a role in calcium regulation and bone
CC   homeostasis.
-!- SUBUNIT: Homodimer; disulfide-linked.
-!- TISSUE SPECIFICITY: EXPRESSED IN THE KIDNEYS AND BLADDER. LOWER
CC   LEVELS SEEN IN THE BRAIN.
-!- SIMILARITY: Belongs to the TGF-beta family.
-!-----------------------------------------------------------------------
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-!-----------------------------------------------------------------------
DR   EMBL; X51801; CAA36100.1; -.
DR   EMBL; M60316; AAA36738.1; -.
DR   EMBL; AL122058; CAB90273.1; -.
DR   EMBL; AL157414; CAC08434.1; -.
DR   EMBL; BC008584; AAH08584.1; -.
DR   PIR; C39263; BMHU7.
DR   PDB; 1BMP; 23-JUL-97.
DR   PDB; 1M4U; 18-DEC-02.
DR   Genew; HGNC:1074; BMP7.
DR   MIM; 112267; -.
DR   GO; GO:0001501; P:skeletal development; TAS.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   ProDom; PD003357; TGFb; 1.
DR   SMART; SM00204; TGFb; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
KW   Signal; Growth factor; Cytokine; Osteogenesis; Chondrogenesis;
KW   Glycoprotein; 3D-structure.
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FT   SIGNAL         1     29
FT   PROPEP        30    292
FT   CHAIN        293    431       BONE MORPHOGENETIC PROTEIN 7.
FT   DISULFID     187    187       INTERCHAIN.
FT   DISULFID     302    302
FT   DISULFID     330    396
FT   DISULFID     359    428
FT   CARBOHYD     321    321       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     329    329       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     363    363       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     372    372       N-LINKED (GLCNAC...) (POTENTIAL).
FT   STRAND       331    333
FT   STRAND       336    338
FT   HELIX        339    342
FT   TURN         343    347
FT   STRAND       348    350
FT   STRAND       353    355
FT   STRAND       358    360
FT   STRAND       362    362
FT   TURN         370    371
FT   HELIX        375    386
FT   HELIX        388    390
FT   HELIX        396    409
FT   STRAND       411    413
FT   STRAND       415    431
FT   POTENTIAL.
FT   POTENTIAL.
SQ   SEQUENCE   431 AA;  49313 MW;  47A05E45C6815F8A CRC64;
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Query Match          100.0%;  Score 111;  DB 1;  Length 431;
Best Local Similarity 100.0%;  Pred. No. 2.9e-09;
Matches  20;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   386 INPETVPKPCCAPTQLNAIS 405
         ||||||||||||||||||||
Db     1 INPETVPKPCCAPTQLNAIS 20
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```
RESULT 2
BMP7_MOUSE
ID   BMP7_MOUSE   STANDARD;   PRT;   430 AA.
AC   P23359; Q91XF7;
DT   01-NOV-1991 (Rel. 20, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Bone morphogenetic protein 7 precursor (BMP-7) (Osteogenic protein 1)
DE   (OP-1).
GN   BMP7 OR BMP-7 OR OP1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon;
RX   MEDLINE=91354237; PubMed=1715687;
RA   Oezkaynak E., Schnegelsberg P.N.J., Oppermann H.;
RT   "Murine osteogenic protein (OP-1): high levels of mRNA in kidney.";
RL   Biochem. Biophys. Res. Commun. 179:116-123(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
```

Left column

RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Induces cartilage and bone formation. May be the
CC   osteoinductive factor responsible for the phenomenon of epithelial
CC   osteogenesis. Plays a role in calcium regulation and bone
CC   homeostasis.
CC   -!- SUBUNIT: Homodimer; disulfide-linked.
CC   -!- SIMILARITY: Belongs to the TGF-beta family.
CC   --
DR   EMBL; X56906; CAA40222.1; -.
DR   EMBL; BC010771; AAH10771.1; -.
DR   HSSP; P18075; 1BMP.
DR   MGD; MGI:103302; Bmp7.
DR   GO; GO:0005615; C:extracellular space; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0005515; F:protein binding; IDA.
DR   GO; GO:0007411; P:axon guidance; IDA.
DR   GO; GO:0009887; P:organogenesis; IMP.
DR   GO; GO:0007389; P:pattern specification; IMP.
DR   GO; GO:0007435; P:salivary gland morphogenesis; IMP.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
KW   Signal; Growth factor; Cytokine; Osteogenesis;
KW   Glycoprotein.
FT   SIGNAL   1   29
FT   PROPEP   30   291   POTENTIAL.
FT   CHAIN   292   430   BONE MORPHOGENETIC PROTEIN 7.
FT   DISULFID   329   395   BY SIMILARITY.
FT   DISULFID   358   427   BY SIMILARITY.
FT   DISULFID   362   429   BY SIMILARITY.
FT   DISULFID   394   394   INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD   186   186   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   301   301   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   320   320   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   371   371   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CONFLICT   167   167   A -> R (IN REF. 1).
SQ   SEQUENCE   430 AA; 49198 MW; 464F36D5D2E54041 CRC64;

Qy   1 INPETVPKPCCAPTQLNAIS 20
               ||| ||||||||||||||||
Db   385 INPDTVPKPCCAPTQLNAIS 404

Query Match   97.3%; Score 108; DB 1; Length 430;
Best Local Similarity   95.0%; Pred. No. 8e-09;
  Matches   19; Conservative   1; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
BMP7_XENLA
ID   BMP7_XENLA   STANDARD;   PRT;   426 AA.
AC   P30086; Q91645;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Bone morphogenetic protein 7 precursor (BMP-7) (Osteogenic protein 1)

Right column

DE   (OP-1) (XBMP7).
GN   BMP7.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92378616; PubMed=1510675;
RA   Nishimatsu S., Suzuki A., Shoda A., Murakami K., Ueno N.;
RT   "Genes for bone morphogenetic proteins are differentially transcribed
RT   in early amphibian embryos.";
RL   Biochem. Biophys. Res. Commun. 186:1487-1495(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Hawley S.H.B., Wunnenberg-Stapleton K., Hashimoto C.,
RA   Laurent M.N., Watabe T., Blumberg B.W., Cho K.W.Y.;
RL   Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Induces cartilage and bone formation. May be the
CC   osteoinductive factor responsible for the phenomenon of epithelial
CC   osteogenesis. Plays a role in calcium regulation and bone
CC   homeostasis.
CC   -!- SUBUNIT: Homodimer; disulfide-linked.
CC   -!- SIMILARITY: Belongs to the TGF-beta family.
CC   --
DR   EMBL; X63427; CAA45021.1; -.
DR   EMBL; U38559; AAA82616.1; -.
DR   PIR; JH0690; JH0690.
DR   HSSP; P18075; 1BMP.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
KW   Signal; Growth factor; Cytokine; Osteogenesis; Chondrogenesis;
KW   Glycoprotein.
FT   SIGNAL   1   22
FT   PROPEP   23   282   POTENTIAL.
FT   CHAIN   283   426   BONE MORPHOGENETIC PROTEIN 7.
FT   DISULFID   325   391   BY SIMILARITY.
FT   DISULFID   354   423   BY SIMILARITY.
FT   DISULFID   358   425   BY SIMILARITY.
FT   DISULFID   390   390   INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD   177   177   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   307   307   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   367   367   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CONFLICT   317   319   KRR -> NVV (IN REF. 2).
FT   CONFLICT   355   355   D -> E (IN REF. 2).
SQ   SEQUENCE   426 AA; 48965 MW; 6401D5151AC97117 CRC64;

Qy   1 INPETVPKPCCAPTQLNAIS 20
               ||| ||||||||||||||| |
Db   381 INPDTVPKPCCAPTQLNGIS 400

Query Match   96.4%; Score 107; DB 1; Length 426;
Best Local Similarity   95.0%; Pred. No. 1.1e-08;
  Matches   19; Conservative   0; Mismatches 1; Indels 0; Gaps 0;

RESULT 4
BMP6_RAT
ID   BMP6_RAT   STANDARD;   PRT;   207 AA.

```
AC   Q04906;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Bone morphogenetic protein 6 precursor (BMP-6) (VG-1-related protein)
DE   (VGR-1) (Fragment).
GN   BMP6 OR BMP-6 OR VGR.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Lewis; TISSUE=Brain;
RX   MEDLINE=93085758; PubMed=1453478;
RA   Sauermann U., Meyermann R., Schluesener H.J.;
RT   "Cloning of a novel TGF-beta related cytokine, the vgr, from rat
RT   brain: Cloning of and comparison to homologous human cytokines.";
RL   J. Neurosci. Res. 33:142-147(1992).
CC   -!- FUNCTION: Induces cartilage and bone formation (By similarity).
CC   -!- SIMILARITY: Belongs to the TGF-beta family.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; X58830; CAA41634.1; -.
DR   PIR; S37618; S37618.
DR   HSSP; P18075; 1BMP.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD003357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
KW   Growth factor; Cytokine; Osteogenesis; Chondrogenesis; Glycoprotein.
FT   NON_TER       1      1
FT   PROPEP       <1     75       POTENTIAL.
FT   CHAIN        76    207       BONE MORPHOGENETIC PROTEIN 6.
FT   DISULFID    106    172       BY SIMILARITY.
FT   DISULFID    135    204       BY SIMILARITY.
FT   DISULFID    139    206       BY SIMILARITY.
FT   DISULFID    171    171       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD     80     80       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     98     98       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    148    148       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   207 AA;  23225 MW;  D5D83C89D8213F51 CRC64;
```

```
GN   BMP6 OR BMP-6 OR VGR1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=94375533; PubMed=8089189;
RA   Gitelman S.E., Kobrin M.S., Ye J.Q., Lopez A.R., Lee A., Derynck R.;
RT   "Recombinant Vgr-1/BMP-6-expressing tumors induce fibrosis and
RT   endochondral bone formation in vivo.";
RL   J. Cell Biol. 126:1595-1609(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=97222480; PubMed=9069123;
RA   Gitelman S.E., Kobrin M., Lee A., Fet V., Lyons K., Hogan B.L.M.,
RA   Derynck R.;
RT   "Structure and sequence of the mouse Bmp6 gene.";
RL   Mamm. Genome 8:212-214(1997).
RN   [3]
RP   SEQUENCE OF 73-510 FROM N.A.
RX   MEDLINE=89282810; PubMed=2734307;
RA   Lyons K., Graycar J.L., Lee A., Hashmi S., Lindquist P.B., Chen E.Y.,
RA   Hogan B.L.M., Derynck R.;
RT   "Vgr-1, a mammalian gene related to Xenopus Vg-1, is a member of the
RT   transforming growth factor beta gene superfamily.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:4554-4558(1989).
CC   -!- FUNCTION: Induces cartilage and bone formation (By similarity).
CC   -!- TISSUE SPECIFICITY: Expressed in the lung. Low levels seen in the
CC       kidney.
CC   -!- SIMILARITY: Belongs to the TGF-beta family.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; X80992; CAA56917.1; -.
DR   EMBL; U73520; AAB18235.1; -.
DR   EMBL; U73515; AAB18235.1; JOINED.
DR   EMBL; U73516; AAB18235.1; JOINED.
DR   EMBL; U73517; AAB18235.1; JOINED.
DR   EMBL; U73518; AAB18235.1; JOINED.
DR   EMBL; U73519; AAB18235.1; JOINED.
DR   EMBL; J04566; AAA40548.1; -.
DR   PIR; A54798; A54798.
DR   HSSP; P18075; 1BMP.
DR   MGD; MGI:88182; Bmp6.
DR   InterPro; IPR002405; Inhibin_alpha.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   PRINTS; PR00669; INHIBINA.
DR   ProDom; PD003357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
KW   Signal; Growth factor; Cytokine; Osteogenesis; Chondrogenesis;
KW   Glycoprotein.
FT   SIGNAL        1     20
FT   PROPEP       21    378       POTENTIAL.
FT   CHAIN       379    510       BONE MORPHOGENETIC PROTEIN 6.
FT   DISULFID    409    475       BY SIMILARITY.
FT   DISULFID    438    507       BY SIMILARITY.
FT   DISULFID    442    509       BY SIMILARITY.
FT   DISULFID    474    474       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    238    238       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    266    266       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    383    383       N-LINKED (GLCNAC...) (POTENTIAL).
```

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RESULT 5
BMP6_MOUSE
ID   BMP6_MOUSE     STANDARD;      PRT;   510 AA.
AC   P20722;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Bone morphogenetic protein 6 precursor (BMP-6) (VG-1-related protein)
DE   (VGR-1).

Query Match             87.4%;  Score 97;  DB 1;  Length 207;
Best Local Similarity   85.0%;
Matches   17;  Conservative    2;  Mismatches   1;  Indels    0;  Gaps    0;

Qy        1 INPEIVPKPCCAPTQLNAIS 20
            :||||||||||||||:|:||||
Db      162 MNPEVVPKPCCAPTLNAIS 181
```

RESULT 6

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ID   BMP6_HUMAN     STANDARD;      PRT;   513 AA.
AC   P22004;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Bone morphogenetic protein 6 precursor (BMP-6).
GN   BMP6 OR VGR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bone;
RX   MEDLINE=91088608; PubMed=2263636;
RA   Celeste A.J., Iannazzi J.A., Taylor R.C., Hewick R.M., Rosen V.,
RA   Wang E.A., Wozney J.M.;
RT   "Identification of transforming growth factor beta family members
RT   present in bone-inductive protein purified from bovine bone.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:9843-9847(1990).
CC   -!- FUNCTION: Induces cartilage and bone formation.
CC   -!- SIMILARITY: Belongs to the TGF-beta family.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; M60315; AAA36737.1; -.
DR   PIR; B39263; BMHU6.
DR   HSSP; P18075; 1BMP.
DR   Genew; HGNC:1073; BMP6.
DR   MIM; 112266; -.
DR   GO; GO:0001501; P:skeletal development; TAS.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
KW   Signal; Growth factor; Cytokine; Osteogenesis; Chondrogenesis;
KW   Glycoprotein.
FT   SIGNAL        1     20
FT   PROPEP       21    381       POTENTIAL.
FT   CHAIN       382    513       BONE MORPHOGENETIC PROTEIN 6.
FT   DISULFID    412    478       BY SIMILARITY.
FT   DISULFID    441    510       BY SIMILARITY.
FT   DISULFID    445    512       BY SIMILARITY.
FT   DISULFID    477    477       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    241    241       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    269    269       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    401    401       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    451    451       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CONFLICT     73     73       K -> M (IN REF. 3).
FT   CONFLICT     75     75       E -> K (IN REF. 3).
FT   CONFLICT     86     86       L -> P (IN REF. 3).
SQ   SEQUENCE   513 AA;  56431 MW;  910B6853128FC2D2 CRC64;
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Qy   465 MNPEYVPKPCCAPTKLNAIS 484
           ::||||||||||:|||:|||
Db   1 INPETVPKPCCAPTQLNAIS 20

Query Match   87.4%; Score 97; DB 1; Length 510;
Best Local Similarity   85.0%;
Matches   17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy   465 MNPEYVPKPCCAPTKLNAIS 484

RESULT 7

```
ID   BMP5_MOUSE     STANDARD;      PRT;   452 AA.
AC   P49003;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Bone morphogenetic protein 5 precursor (BMP-5).
GN   BMP5 OR BMP-5.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C3H/KW;
RX   MEDLINE=95046894; PubMed=7958439;
RA   King J.A., Marker P.C., Seung K.J., Kingsley D.M.;
RT   "BMP5 and the molecular, skeletal, and soft-tissue alterations in
RT   short ear mice.";
RL   Dev. Biol. 166:112-122(1994).
CC   -!- FUNCTION: Induces cartilage and bone formation.
CC   -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC   -!- SIMILARITY: Belongs to the TGF-beta family.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; L41145; AAA64612.1; -.
DR   PIR; I49542; I49542.
DR   HSSP; P18075; 1BMP.
DR   MGD; MGI:88181; Bmp5.
DR   GO; GO:0007389; P:pattern specification; IMP.
DR   GO; GO:0001501; P:skeletal development; IMP.
DR   InterPro; IPR024400; GF_cysknot.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
KW   Signal; Growth factor; Cytokine; Osteogenesis; Chondrogenesis;
KW   Glycoprotein.
FT   SIGNAL        1     25
FT   PROPEP       26    320       POTENTIAL.
FT   CHAIN       321    452       BONE MORPHOGENETIC PROTEIN 5.
FT   DISULFID    351    417       BY SIMILARITY.
FT   DISULFID    380    449       BY SIMILARITY.
FT   DISULFID    384    451       BY SIMILARITY.
FT   DISULFID    416    416       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    209    209       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    325    325       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    386    386       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    404    404       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    454    454       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   452 AA;  57225 MW;  3F19155B3C049278 CRC64;
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Qy   468 MNPEYVPKPCCAPTKLNAIS 487
           ::||||||||||:|||:|||
Db   1 INPETVPKPCCAPTQLNAIS 20

Query Match   87.4%; Score 97; DB 1; Length 513;
Best Local Similarity   85.0%;
Matches   17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy   468 MNPEYVPKPCCAPTKLNAIS 487

Qy   3 PETVPKPCCAPTQLNAIS 20
           :|||||||||||||:||||
Db   409 PDHVPKPCCAPTKLNAIS 426

RESULT 8
ID   BMP5_HUMAN   STANDARD;   PRT;   454 AA.
AC   P22003; Q9H547; Q9NTM5;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Bone morphogenetic protein 5 precursor (BMP-5).
GN   BMP5.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bone;
RX   MEDLINE=91088608; PubMed=2263636;
RA   Celeste A.J., Iannazzi J.A., Taylor R.C., Hewick R.M., Rosen V.,
RA   Wang E.A., Wozney J.M.;
RT   "Identification of transforming growth factor beta family members
RT   present in bone-inductive protein purified from bovine bone.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:9843-9847(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Bates K., Tracey A.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung, and Spleen;
RX   MEDLINE=22382257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Induces cartilage and bone formation.
CC   -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC   -!- TISSUE SPECIFICITY: Expressed in the lung and liver.
CC   -!- SIMILARITY: Belongs to the TGF-beta family.
CC   --

CC   entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; M60314; AAA36736.1; -.
DR   EMBL; AL137178; CAC12766.1; -.
DR   EMBL; AL133386; CAB91657.1; -.
DR   EMBL; BC027958; AAH27958.1; -.
DR   PIR; A39263; BMHU5.
DR   HSSP; P18075; 1BMP.
DR   Genew; HGNC:1072; BMP5.
DR   MIM; 112265; -.
DR   GO; GO:0005125; F:cytokine activity; NAS.
DR   GO; GO:0001501; P:skeletal development; NAS.
DR   InterPro; IPR002400; GF_Cysknot.
DR   InterPro; IPR001839; TGFB.
DR   InterPro; IPR001111; TGFB_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   PRINTS; PF00438; GFCYSKNOT.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
KW   Signal; Growth factor; Cytokine; Osteogenesis; Chondrogenesis;
KW   Glycoprotein.
FT   SIGNAL   1   30   POTENTIAL.
FT   PROPEP   31   322   POTENTIAL.
FT   CHAIN   323   454   BONE MORPHOGENETIC PROTEIN 5.
FT   DISULFID   353   419   BY SIMILARITY.
FT   DISULFID   382   451   BY SIMILARITY.
FT   DISULFID   386   453   BY SIMILARITY.
FT   DISULFID   418   418   INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD   211   211   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   327   327   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   345   345   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   395   395   N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   454 AA; 51736 MW; 631277413CCC22EE CRC64;

Qy   3 PETVPKPCCAPTQLNAIS 20
           :|||||||||||||:||||
Db   411 PDHVPKPCCAPTKLNAIS 428

RESULT 9
ID   60A_DROVI   STANDARD;   PRT;   436 AA.
AC   Q24735;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   60A protein precursor (Glass bottom boat protein).
GN   GBB OR 60A OR TGFB-60A.
OS   Drosophila virilis (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydridea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7244;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96305349; PubMed=8688461;
RA   Du W., Doctor J.S.;
RT   "Isolation and sequence of the Drosophila virilis 60 A gene, a
RT   transforming growth factor-beta superfamily member related to
RT   vertebrate bone morphogenetic proteins.";
RL   Biochim. Biophys. Acta 1307:273-279(1996).
CC   -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC   -!- SIMILARITY: Belongs to the TGF-beta family.
CC   --

Query Match   78.4%;   Score 87;   DB 1;   Length 452;
Best Local Similarity   83.3%;   Pred. No. 1.2e-05;
Matches   15;   Conservative   2;   Mismatches   1;   Indels   0;   Gaps   0;

Query Match   78.4%;   Score 87;   DB 1;   Length 454;
Best Local Similarity   83.3%;   Pred. No. 1.2e-05;
Matches   15;   Conservative   2;   Mismatches   1;   Indels   0;   Gaps   0;

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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; U48595; AAC47262.1; -.
DR   HSSP; P18075; 1BMP.
DR   FlyBase; FBgn0015681; Dvir\gbb.
DR   InterPro; IPR002400; GF cysknot.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb propeptide; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF BETA 1; 1.
KW   Growth factor; Cytokine; Glycoprotein; Signal.
FT   SIGNAL        1     27       POTENTIAL.
FT   PROPEP       28    317       POTENTIAL.
FT   CHAIN       318    436       60A PROTEIN.
FT   DISULFID    335    401       BY SIMILARITY.
FT   DISULFID    364    433       BY SIMILARITY.
FT   DISULFID    368    435       BY SIMILARITY.
FT   DISULFID    400    400       INTERCHAIN (BY SIMILARITY).
FT   DISULFID    400    400       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    102    102       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    114    114       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    217    217       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    229    229       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    377    377       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   436 AA;  49999 MW;  C744B4AE58796692 CRC64;

Qy          1 INPETVRKPCCAPTQLNAI 19
              : .|:|||||.|||||.|
Db        391 LEPRVPKPCCAPTRLGAL 409

RESULT 10
60A_DROME

Query Match             69.4%;
Best Local Similarity   63.2%;
Matches   12;  Conservative    4;

Score 77;  DB 1;  Length 436;
Pred. No. 0.00035;
Mismatches    3;  Indels    0;  Gaps    0;

ID   60A_DROME     STANDARD;      PRT;   455 AA.
AC   P27091; Q9W114;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   60A protein precursor (Glass bottom boat protein).
GN   GBB OR 60A OR TGFB-60A OR CG5562.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92021021; PubMed=1924384;
RA   Wharton K.A., Thomsen G.H., Gelbart W.M.;
RT   "Drosophila 60A gene, another transforming growth factor beta family
RT   member is closely related to human bone morphogenetic proteins.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:9214-9218(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92290120; PubMed=1601181;
RA   Doctor J.S., Jackson P.D., Rashka K.E., Visalli M., Hoffmann F.M.;
RT   "Sequence, biochemical characterization, and developmental expression
RT   of a new member of the TGF-beta superfamily in Drosophila
RT   melanogaster.";
RL   Dev. Biol. 151:491-505(1992).
RN   [3]
RP   SEQUENCE FROM N.A.
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RC   STRAIN=Berkeley;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
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CC   -!- SUBUNIT: Homodimer; disulfide-linked.
CC   -!- DEVELOPMENTAL STAGE: Expressed throughout development with peaks
CC       of transcription during early embryogenesis, in pupae, and in
CC       adult males.
CC   -!- SIMILARITY: Belongs to the TGF-beta family.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; M77012; AAA28306.1; -.
DR   EMBL; M84795; AAA28307.1; -.
DR   EMBL; AE003462; AAF47075.1; -.
DR   PIR; A43918; A43918.
DR   HSSP; P18075; 1BMP.
DR   FlyBase; FBgn0024234; gbb.
DR   GO; GO:0008586; P:wing morphogenesis; IMP.
DR   GO; GO:0007474; P:wing vein specification; IMP.
DR   InterPro; IPR002400; GF cysknot.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb propeptide; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF BETA 1; 1.
KW   Growth factor; Cytokine; Glycoprotein; Signal.
FT   SIGNAL        1     36       POTENTIAL.
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FT   PROPEP   37   335   POTENTIAL.
FT   CHAIN   336   455   60A PROTEIN.
FT   DISULFID   354   420   BY SIMILARITY.
FT   DISULFID   383   452   BY SIMILARITY.
FT   DISULFID   387   454   BY SIMILARITY.
FT   DISULFID   419   419   INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD   238   238   N-LINKED (GlcNAc...) (POTENTIAL).
FT   CARBOHYD   250   250   N-LINKED (GlcNAc...) (POTENTIAL).
FT   CARBOHYD   396   396   N-LINKED (GlcNAc...) (POTENTIAL).
FT   SEQUENCE   455 AA; 51687 MW; C8FA79555634lF94 CRC64;

Qy
Query Match   69.4%; Score 77; DB 1; Length 455;
Best Local Similarity   63.2%; Pred. No. 0.00036;
Matches   12; Conservative   4; Mismatches   3; Indels   0; Gaps   0;

Qy   1 INPETVPKPCCAPTQLNAI 19
             |:|||||||||||:|:|:
Db   410 LEPKKVPKPCCAPTRIGAL 428

RESULT 11
ID   BM8A_MOUSE   STANDARD;   PRT;   399 AA.
AC   P34821;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Bone morphogenetic protein 8A precursor (BMP-8A) (Osteogenic protein
DE   2) (OP-2).
GN   BMP8A OR BMP-8.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=93094231; PubMed=1460021;
RA   Ozkaynak E., Schnegelsberg P.N.J., Jin D.F., Clifford G.M.,
RA   Warren F.D., Drier E.A., Oppermann H.;
RT   "Osteogenic protein-2. A new member of the transforming growth
RT   factor-beta superfamily expressed early in embryogenesis.";
RL   J. Biol. Chem. 267:25220-25227(1992).
CC   -!- FUNCTION: Induces cartilage and bone formation. May be the
CC   osteoinductive factor responsible for the phenomenon of epithelial
CC   osteogenesis. Plays a role in calcium regulation and bone
CC   homeostasis (By similarity).
CC   -!- SUBUNIT: Homodimer; disulfide-linked.
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- DEVELOPMENTAL STAGE: EXTENSIVE EXPRESSION FOUND IN 8-DAY EMBRYOS,
CC   FELL DRASTICALLY IN 10-DAY EMBRYOS AND VIRTUALLY ABSENT IN 17-
CC   DAY EMBRYOS.
CC   -!- SIMILARITY: Belongs to the TGF-beta family.

DR   EMBL; M97017; AAB01365.1; -.
DR   HSSP; P18075; 1BMP.
DR   MGD; MGI:104515; Bmp8a.
DR   GO; GO:0007283; P:spermatogenesis; IMP.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD000357; TGFB; 1.

DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
KW   Signal; Growth factor; Cytokine; Osteogenesis; Chondrogenesis;
KW   Glycoprotein.
FT   SIGNAL   1   19   POTENTIAL.
FT   PROPEP   20   260   POTENTIAL.
FT   CHAIN   261   399   BONE MORPHOGENETIC PROTEIN 8A.
FT   DISULFID   298   364   BY SIMILARITY.
FT   DISULFID   327   396   BY SIMILARITY.
FT   DISULFID   331   398   BY SIMILARITY.
FT   DISULFID   363   363   INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD   155   155   N-LINKED (GlcNAc...) (POTENTIAL).
FT   CARBOHYD   340   340   N-LINKED (GlcNAc...) (POTENTIAL).
FT   SEQUENCE   399 AA; 44764 MW; B75FE332D6125B40C CRC64;

Qy
Query Match   64.9%; Score 72; DB 1; Length 399;
Best Local Similarity   60.0%; Pred. No. 0.0018;
Matches   12; Conservative   4; Mismatches   4; Indels   0; Gaps   0;

Qy   1 INPETVPKPCCAPTQLNAIS 20
             |:|||||||||||:|:|:
Db   354 MKPDVVPKACCAPTKLSATS 373

RESULT 12
ID   DECA_DROPS   STANDARD;   PRT;   621 AA.
AC   P91699;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Decapentaplegic protein precursor (DPP-C protein).
GN   DPP.
OS   Drosophila pseudoobscura (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7237;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97225212; PubMed=9071585;
RA   Newfeld S.J., Padgett R.W., Findley S.D., Richter B.G., Sanicola M.,
RA   de Cuevas M., Gelbart W.M.;
RT   "Molecular evolution at the decapentaplegic locus in Drosophila.";
RL   Genetics 145:297-309(1997).
CC   -!- FUNCTION: ACTS AS AN EXTRACELLULAR MORPHOGEN TO ESTABLISH AT LEAST
CC   TWO CELLULAR RESPONSE THRESHOLDS WITHIN THE DORSAL HALF OF THE
CC   DROSOPHILA EMBRYO. REQUIRED FOR THE PROPER DEVELOPMENT OF THE
CC   DROSOPHILA DORSAL HYPODERM, FOR VIABILITY OF LARVAE AND FOR CELL
CC   VIABILITY OF THE EPITHELIAL CELLS IN THE IMAGINAL DISKS. ACTS
CC   TOGETHER WITH SCW (BY SIMILARITY).
CC   -!- SUBUNIT: HETERODIMERS OF SCW/DPP ARE THE ACTIVE SUBUNIT, DPP/DPP
CC   HOMODIMERS ELICIT A BASAL RESPONSE AND SCW/SCW HOMODIMERS ALONE
CC   ARE INEFFECTIVE IN SPECIFYING A DORSAL PATTERN (BY SIMILARITY).
CC   -!- TISSUE SPECIFICITY: Expressed in the imaginal discs associated
CC   with establishment of the proximal-distal axis of the appendages,
CC   and midgut mesoderm (By similarity).
CC   -!- SIMILARITY: Belongs to the TGF-beta family.

DR   EMBL; U63856; AAC47553.1; -.
DR   HSSP; P12643; 3BMP.
DR   FlyBase; FBgn0018547; Dpse\dpp.
DR   InterPro; IPR002405; Inhibin_alpha.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.

DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   PRINTS; PD00669; INHIBINA.
DR   ProDom; PD00357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
KW   Growth factor; Developmental protein; Differentiation; Glycoprotein;
KW   Signal.
FT   SIGNAL   1   15   POTENTIAL.
FT   PROPEP   16   479   BY SIMILARITY.
FT   CHAIN   480   621   DECAPENTAPLEGIC PROTEIN.
FT   DISULFID   520   586   BY SIMILARITY.
FT   DISULFID   549   618   BY SIMILARITY.
FT   DISULFID   553   620   BY SIMILARITY.
FT   DISULFID   585   585   INTERCHAIN (BY SIMILARITY).
FT   DOMAIN   45   57   POLY-ALA.
FT   DOMAIN   88   92   POLY-ASN.
FT   DOMAIN   95   104   POLY-ASN.
FT   DOMAIN   163   173   POLY-GLN.
FT   DOMAIN   483   495   POLY-GLY.
FT   CARBOHYD   149   149   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   365   365   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   400   400   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   562   562   N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   621 AA; 69038 MW; 3FD7141FB5509651 CRC64;

Qy   1 INPETVPKPCCAPTQLNAIS 20
                 |||:||||||||||||||:::
Db   576 LNPGKVPKACCVPTQLDSVA 595

RESULT 13
ID   DVR1_XENLA   STANDARD;   PRT;   360 AA.
AC   P09534;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-MAR-1989 (Rel. 10, Last sequence update)
DT   01-JUN-1994 (Rel. 29, Last annotation update)
DE   DVR-1 protein precursor (Vegetal hemisphere VG1 protein) (VG-1).
GN   DVR-1 OR VG1.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88052889; PubMed=3479264;
RA   Weeks D.L., Melton D.A.;
RT   "A maternal mRNA localized to the vegetal hemisphere in Xenopus eggs
RT   codes for a growth factor related to TGF-beta.";
RL   Cell 51:861-867(1987).
RN   [2]
RX   CARBOHYDRATE-LINKAGE SITES.
RX   MEDLINE=89305504; PubMed=2519512;
RA   Dale L., Matthews G., Tabe L., Colman A.;
RT   "Developmental expression of the protein product of Vg1, a localized
RT   maternal mRNA in the frog Xenopus laevis.";
RL   EMBO J. 8:1057-1065(1989).
CC   -!- FUNCTION: SERVES TO FACILITATE THE DIFFERENTIATION OF EITHER
CC   MESODERM OR ENDODERM EITHER AS A COFACTOR IN AN INSTRUCTIVE
CC   SIGNAL OR BY PROVIDING PERMISSIVE ENVIRONMENT.
CC   -!- SUBUNIT: Homodimer (Probable).
CC   -!- TISSUE SPECIFICITY: VEGETAL REGION OF THE EGG.
CC   -!- DEVELOPMENTAL STAGE: ABUNDANT IN OOCYTES AND PRESENT THROUGHOUT
CC   CLEAVAGE AND GASTRULA STAGE. NOT READILY DETECTED AT A STAGE WHEN
CC   SOMITOGENESIS IS NEARLY COMPLETE IN 24 HR EMBRYOS. STEADY STATE
CC   LEVEL DECREASES IN A CONTINOUS FASHION WITH DEVELOPMENTAL AGE.
CC   -!- SIMILARITY: Belongs to the TGF-beta family.

CC   ---
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CC   or send an email to license@isb-sib.ch).
CC   ---
DR   EMBL; M18055; AAA49727.1; -.
DR   PIR; A29619; A29619.
DR   HSSP; P12643; 3BMP.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR002405; Inhibin_alpha.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   PRINTS; PR00669; INHIBINA.
DR   ProDom; PD00357; TGFb; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
KW   Growth factor; Mitogen; Glycoprotein; Signal.
FT   SIGNAL   1   16   POTENTIAL.
FT   PROPEP   17   246
FT   CHAIN   247   360   DVR-1 PROTEIN.
FT   DISULFID   259   325   BY SIMILARITY.
FT   DISULFID   288   357   BY SIMILARITY.
FT   DISULFID   292   359   BY SIMILARITY.
FT   DISULFID   324   324   INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD   113   113   N-LINKED (GLCNAC...).
FT   CARBOHYD   181   181   N-LINKED (GLCNAC...).
FT   CARBOHYD   301   301   N-LINKED (GLCNAC...).
SQ   SEQUENCE   360 AA; 41772 MW; E444A18AA2750984 CRC64;

Qy   1 INPETVPKPCCAPTQLNAIS 20
                 |:|||||||||||||||||||
Db   315 IEPEDILPCCVPTKMSPIS   334

RESULT 14
ID   BM8B_MOUSE   STANDARD;   PRT;   399 AA.
AC   P55105;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Bone morphogenetic protein 8B precursor (BMP-8B).
GN   BMP8B
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ICR; TISSUE=Placenta;
RX   MEDLINE=97000308; PubMed=8843393;
RA   Zhao G.Q., Hogan B.L.;
RT   "Evidence that mouse Bmp8a (Op2) and Bmp8b are duplicated genes that
RT   play a role in spermatogenesis and placental development.";
RL   Mech. Dev. 57:159-168(1996).
CC   -!- FUNCTION: Induces cartilage and bone formation. May be the
CC   osteoinductive factor responsible for the phenomenon of epithelial
CC   osteogenesis. Plays a role in calcium regulation and bone
CC   homeostasis (By similarity).
CC   -!- SUBUNIT: Homodimer; disulfide-linked.
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- SIMILARITY: Belongs to the TGF-beta family.

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CC   or send an email to license@isb-sib.ch).
CC   ---
DR   EMBL; U39545; AAB17573.1; -.
DR   HSSP; P18075; 1BMP.
DR   MGD; MGI:107335; Bmp8b.
DR   GO; GO:0007283; P:spermatogenesis; IMP.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFb; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
KW   Signal; Growth factor; Cytokine; Osteogenesis; Chondrogenesis;
KW   Glycoprotein.
FT   SIGNAL   1   19   POTENTIAL.
FT   PROPEP   20   260   POTENTIAL.
FT   CHAIN   261   399   BONE MORPHOGENETIC PROTEIN 8B.
FT   DISULFID   298   364   BY SIMILARITY.
FT   DISULFID   327   396   BY SIMILARITY.
FT   DISULFID   331   398   BY SIMILARITY.
FT   DISULFID   363   363   INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD   155   155   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   340   340   N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   399 AA; 44752 MW; EFA0B7B8C7EC4839 CRC64;

Qy   1 INPETVRPCCAPTQLNAIS 20
                 : ::   ::: : ::: :
Db   354 MKPDIIPKVCCVPVPELSAIS 373

Query Match   64.0%; Score 71; DB 1; Length 399;
Best Local Similarity   55.0%;
Matches   11; Conservative   5; Mismatches   4; Indels   0; Gaps   0;
                        Pred. No. 0.0025;

RESULT 15
DECA_DROME

ID   DECA_DROME   STANDARD;   PRT;   588 AA.
AC   P07713; P91651;
DT   01-APR-1988 (Rel. 07, Created)
DT   01-APR-1988 (Rel. 07, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Decapentaplegic protein precursor (DPP-C protein).
GN   DPP.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87090408; PubMed=3467201;
RA   Padgett R.W., St Johnston R.D., Gelbart W.M.;
RT   "A transcript from a Drosophila pattern gene predicts a protein
RT   homologous to the transforming growth factor-beta family.";
RL   Nature 325:81-84(1987).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97225213; PubMed=9071586;
RC   STRAIN=DP CN BW;
RA   Richter B., Long M., Lewontin R.C., Nitasaka E.;
RT   "Nucleotide variation and conservation at the dpp locus, a gene
RT   controlling early development in Drosophila.";
RL   Genetics 145:311-323(1997).
RN   [3]
RP   CHARACTERIZATION, AND SEQUENCE OF 457-476.

RX   MEDLINE=92258853; PubMed=1692958;
RA   Panganiban G.E.F., Rashka K.E., Neitzel M.D., Hoffmann F.M.;
RT   "Biochemical characterization of the Drosophila dpp protein, a member
RT   of the transforming growth factor beta family of growth factors.";
RL   Mol. Cell. Biol. 10:2669-2677(1990).
CC   ---
CC   -!- FUNCTION: ACTS AS AN EXTRACELLULAR MORPHOGEN TO ESTABLISH AT LEAST
CC   TWO CELLULAR RESPONSE THRESHOLDS WITHIN THE DORSAL HALF OF THE
CC   DROSOPHILA EMBRYO. REQUIRED FOR THE PROPER DEVELOPMENT OF THE
CC   EMBRYONIC DORSAL HYPODERM, FOR VIABILITY OF LARVAE AND FOR CELL
CC   VIABILITY OF THE EPITHELIAL CELLS IN THE IMAGINAL DISKS. ACTS
CC   TOGETHER WITH SCW.
CC   -!- SUBUNIT: HETERODIMERS OF SCW/DPP ARE THE ACTIVE SUBUNIT, DPP/DPP
CC   HOMODIMERS ELICIT A BASAL RESPONSE AND SCW/SCW HOMODIMERS ALONE
CC   ARE INEFFECTIVE IN SPECIFYING A DORSAL PATTERN.
CC   -!- TISSUE SPECIFICITY: Expressed in the imaginal discs associated
CC   with establishment of the proximal-distal axis of the appendages,
CC   and midgut mesoderm.
CC   -!- SIMILARITY: Belongs to the TGF-beta family.
CC   ---
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CC   or send an email to license@isb-sib.ch).
CC   ---
DR   EMBL; M30116; AAA28402.1; -.
DR   EMBL; U63857; AAC47552.1; -.
DR   PIR; A26182; A26182.
DR   HSSP; P12643; 3BMP.
DR   FlyBase; FBgn0000490; dpp.
DR   GO; GO:0005615; C:extracellular space; IDA.
DR   GO; GO:0005622; C:intracellular; IDA.
DR   GO; GO:0005615; C:extracellular; IDA.
DR   GO; GO:0016015; F:morphogen activity; NAS.
DR   GO; GO:0005109; F:transforming growth factor-beta receptor bi...; NAS.
DR   GO; GO:0007378; P:amnioserosa formation; NAS.
DR   GO; GO:0007179; P:TGFbeta receptor signaling pathway; NAS.
DR   GO; GO:0007425; P:tracheal cell fate determination (sensu Ins...; NAS.
DR   GO; GO:0008586; P:wing vein morphogenesis; IMP.
DR   GO; GO:0007474; P:wing vein specification; IMP.
DR   GO; GO:0007448; P:anterior/posterior pattern formation; NAS.
DR   GO; GO:0007391; P:dorsal closure; NAS.
DR   GO; GO:0001715; P:ectoderm cell fate specification; NAS.
DR   GO; GO:0001716; P:ectoderm cell fate specification; NAS.
DR   GO; GO:0007442; P:hindgut morphogenesis; IMP.
DR   GO; GO:0007560; P:imaginal disc morphogenesis; NAS.
DR   GO; GO:0007479; P:leg disc proximal/distal pattern formation; NAS.
DR   GO; GO:0042127; P:regulation of cell proliferation; NAS.
DR   GO; GO:0019827; P:stem cell maintenance; NAS.
DR   GO; GO:0007352; P:zygotic determination of dorsal/ventral axis; NAS.
DR   InterPro; IPR024405; Inhibin_alpha.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   PRINTS; PR00669; INHIBINA.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFb; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
KW   Growth factor; Developmental protein; Differentiation; Glycoprotein;
KW   Signal.
FT   SIGNAL   1   15   POTENTIAL.
FT   PROPEP   16   456   POTENTIAL.
FT   CHAIN   457   588   DECAPENTAPLEGIC PROTEIN.
FT   DISULFID   487   553   BY SIMILARITY.
FT   DISULFID   516   585   BY SIMILARITY.
FT   DISULFID   520   587   BY SIMILARITY.
FT   DISULFID   552   552   INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD   120   120   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   342   342   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   377   377   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   529   529   N-LINKED (GLCNAC...) (POTENTIAL).

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FT   VARIANT       59     59      V -> G (IN STRAIN DP CN BW).
FT   VARIANT      121    121      K -> M (IN STRAIN DP CN BW).
FT   VARIANT      473    474      HA -> QP (IN STRAIN DP CN BW).
SQ   SEQUENCE     588 AA;  65850 MW;  3D986A7DF5DF666B CRC64;

     Query Match          64.0%;  Score 71;  DB 1;  Length 588;
     Best Local Similarity  55.0%;  Pred. No. 0.0037;
     Matches   11;  Conservative   5;  Mismatches   4;  Indels   0;  Gaps   0;

Qy        1  INPETVPKPCCAPTQLNAIS 20
             : ||  ||||  || |||::::
Db      543  MNPGKVPKACCVPIQLDSVA 562
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